

STIC-Biotech/ChemLib

From: Slobodyansky, Elizabeth
Sent: Tuesday, November 27, 2001 7:01 PM
To: STIC-Biotech/ChemLib
Subject: 09/590,375

Please search for case 09/590,375:

SEQ ID NOs: 1 and 2 against protein, DNA ~~and interference~~ databases.

Thank you.

Elizabeth Slobodyansky, PhD
Primary Examiner

AU 1652
CM1-10D11
tel. 306-3222

mail box 10C01

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: 11/30/01
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST(where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

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56 1g1yrg1yAlATyAspleuTyAspleuGlyluPheasnGlnlysg 73
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47 .GGCTACGAGCTCTACGATCTGTATGATCGGGCCAGTGTGACCAAG 95
   ||||| .....
73 1yhrValArgThrlyTyrglyThrArgserGlnleuGlnlyAlaVal 89
   ||||| .....
96 GCTCCAAAGGCGACAGTGGGCCCAAGACCACTGGAGCGAGCTGTC 145
   ||||| .....
90 ThrSerleuYasnAnsglyllleGlnValTyrglyAspValValMet 106
   ||||| .....
146 CGGCGCGCGGGGACGGCGCATTCGATCTGTTGATGCCGCTGAA 195
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106 nh1slyG1yG1yAlAspGlyThrglMetValAsnAlaValAluVal 123
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196 CCACAAAGGCGGGCGGATTCACCGAGCAAGTCTTGCCACGAGGCTG 245
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123 sn.Arg..... 124
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246 ACCGAGAGGTTGTGGCCGTATGTCCTGCGCAAGATCCGTTGTA 295
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125 .....Ser 125
   ||||| .....
236 TCGCATCCGGCTGACAAAGAACTGCCACGCTACTCTGATGTTGCA 345
   ||||| .....
126 AsnArgAsnGlnGluIleSerGlyGluTyThrIleGluAlaTrpThrly 142
   ||||| .....
346 GATCCCGCCANACAGTGCATCGCCGGAGACATCGAGCGCTGACCAA 395
   ||||| .....
142 sPheAspPheProGlyArgGlyAsnThrHisSerAsnPhelyStrArgT 159
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396 GTTCACATCCCGAGCGCATGATCAATATAGCTCCGCGGCTGCAACA 445
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159 rPtyHisPheAspGlyThrAspTrpAspGlnSerArgGlnleuGlnAsn 175
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446 AGCGCATTTTCACAGTGTGACACTGACAAATGCAACTGCT...GAAAG 492
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176 LysIleTyrlsPheArgGlyThrglyysAlaTrpAspTrpGluValAs 192
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493 GCCATATGCTGTTGAG.....GGCAGAAAGTGGCGGAGGATGTCAA 536
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192 rIleGluAsnGlyAsnTyAspTyrlleu..... 201
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537 CGGAGACTTGTGTAATGACTACTGTGAGTCTGAGTCTGAGGAGT 586
   ||||| .....
202 .....MetYrAlaAsp 205
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637 CTAGATCATTCATCTCTGAAGTCAGAGAGTCTTAAAGTGGCCCAA 686
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222 lTrpTyrlThAsnThrleuAsnleuAspGlyPheArgIleAspAlaVal 239
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687 GTGGCTCAACGATCAATGTTGCTGGCGGCTTTCGCTGAGCGCGGTA 736
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239 yshisile 241
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737 AAGCATA 744
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clone NF047G02EC 5', mRNA sequence.
ACCESSION BF648578
VERSION BF648578.1 GI:11913708
KEYWORDS EST.
SOURCE Medicago truncatula
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

```

```

REFERENCE
AUTHORS Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
Medicago.
1 (bases 1 to 665)
Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J.,
Flores, H.R., Iman, J.T., Weller, J.W. and May, G.D.
TITLE Expresed Sequence Tags from the Samuel Roberts Noble Foundation -
Center for Medicago Genomics Research
JOURNAL Unpublished (2000)
COMMENT Contact: Dixon RA
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7302
Fax: 580 221 7380
Email: radixon@noble.org
Insert length: 665 Std Error: 0.00
Plate: 047 row: G column: 02
Seq primer: TCACACGAGAAACGCTATGAC.
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/db_xref="taxon:3880"
/clone_id="NF047G02EC"
/tissue_type="Elicited cell culture"
/dev_stage="Cell suspensions were derived from root tissues"
/dev_stage="Cell suspensions were subcultured every 14
days. Cells were induced six days after subculture"
/note="Vector: Lambda Zap; Cells were induced with yeast
cell wall extracts equivalent to 50ug/ml glucose in the
final concentration. Samples were taken at 0.5, 1, 12 and
24 hours after induction. Equal amounts of RNA from each
time point were pooled and used for mRNA isolation."
BASE COUNT 196 a 131 c 128 g 207 t 3 others
ORIGIN
alignment_scores:
Quality: 202.50 Length: 250
Ratio: 1.594 Gaps: 10
Percent Similarity: 50.800 Percent Identity: 26.400
alignment_block:
US-09-590-375-2 x BF648578 ..
Align seg 1/1 to: BF648578 from: 1 to: 665
13 pheGluTrpHisLeuProAsnAspGlyAsnHisTrpAsnArgLeuArgAs 29
||||| .....
87 TTCAACTGGGAGTCACAGTACCAAGAGAGATGTGACAACTCTTGAGAA 136
||||| .....
29 pAspAlaAlaAsnleuYsserlysgIleThrAlaValTrpIleProp 46
||||| .....
137 CCTCATTCCTGACCTAGCAAAATGCTGGAATTACACAGTTGGCTTC 186
||||| .....
46 roAlaTrpGlyGlyThrSerGlnAsnAspValGlyTyrglyAlaTyAsp 62
||||| .....
187 CT.....CCATCTCAAGTGTGTGCTCAAGGATATCTTCAGAGAGA 230
||||| .....
63 leuTyAspLeuGlyGluPheasnGlnlysglyThrValArgThrlysty 79
||||| .....
231 CTTTATGATCTTGAT.....GCATCAAAATA 256
||||| .....
79 rGlyThrArgserGlnleuGlnlyAlaValThrSerleuYasnAnsg 96
||||| .....
257 CGGTTCAAAGATGACCTAAAGTCACTAATTGACACTTTCAAAGTAAAG 306
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96 lYlIleGlnValTyrglyAspValAlaMetAsnHislyGlyGlyAlaAsp 112
||||| .....
307 GAATCAATGTTGCTAGCTGACATGATCAACCAT..... 341
||||| .....
113 GlyThrGluMetValAsnAlaValGluValAsnArgSerAsnArgAsnG 129
||||| .....
342 .....AGACAGCAGAAAGAAA 358
||||| .....

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129 nguiilesrgluytuythrliegualatprrltylshsapher 146
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359 AGATGATACAGGACATATGCTC...TTTG 387
146 rogluyatrgluyantrhissrfsanphelystrpatgrrtyrhissph 162
    ||| :||| :|||
388 AAGCT...GGACCTCTGATTCAAACCT... 413
163 ASpglYthAsprrAspClnSerArglnLeuGlnAsnlyslleTly 179
414 .....GATGGGGCCCATCTTTCAGAAAGTCACACTGCTTA 454
179 sPhedrglYthrglYsalatrpAsprrglYvalAsprrleGlnsng 196
    ||||| :||| :|||
455 TTGCAGATGGCACTGGA...AACCTGATAGTCG 483
196 lyAsnTYtrAsprrYleuMeTYtrAlaAsprrleAspMetAsprrsPtoGlu 212
484 GAGAC...GGCATATCAAGCTGCACCTGCACATTGATCATCTCAATCCCA 530
213 ValleAsnGluLeuArgAsnTrpGlyValTrpTYthAsnThrLeuAs 229
    ||| :||| :||| ||| :|||
531 GTTCAAAAGAAAGATATCTCAATAGCATGCAATTGGCTCAAAACCTGAAATTGG 580
229 AleuAspGlyPheArglLeaSpAlaVallyshisTleuSTySierTYT 246
581 ATTTCCTGGGTGGAGACTTGTGATTTGTCAAAANGATATCGGCTANCAATA 630
246 hArGrgsPrrPleuThrhIsValArgAsnTrhThGlyLysPrrMePhe 265
531 CAAAA...ATTATATAGGAAATATCTGC...CCANATTYT 665

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seq_name: gb-gss:CNS0100L

seq_documentation_block:

DEFINITION *Anopheles gambiae*

genomic surv

VERSION AL153781.1

SOURCE	African male
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1965-69	1965-69
1970-74	1970-74
1975-79	1975-79
1980-84	1980-84
1985-89	1985-89
1990-94	1990-94
1995-99	1995-99
2000-04	2000-04
2005-09	2005-09
2010-14	2010-14
2015-19	2015-19
2020-24	2020-24
2025-29	2025-29
2030-34	2030-34
2035-39	2035-39
2040-44	2040-44
2045-49	2045-49
2050-54	2050-54
2055-59	2055-59
2060-64	2060-64
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2075-79	2075-79
2080-84	2080-84
2085-89	2085-89
2090-94	2090-94
2095-99	2095-99
2100-04	2100-04
2105-09	2105-09
2110-14	2110-14
2115-19	2115-19
2120-24	2120-24
2125-29	2125-29
2130-34	2130-34
2135-39	2135-39
2140-44	2140-44
2145-49	2145-49
2150-54	2150-54
2155-59	2155-59
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2170-74	2170-74
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2185-89	2185-89
2190-94	2190-94
2195-99	2195-99
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2240-44	2240-44
2245-49	2245-49
2250-54	2250-54
2255-59	2255-59
2260-64	2260-64
2265-69	2265-69
2270-74	2270-74
2275-79	2275-79
2280-84	2280-84
2285-89	2285-89
2290-94	2290-94
2295-99	2295-99
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2355-59	2355-59
2360-64	2360-64
2365-69	2365-69
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2375-79	2375-79
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2470-74	2470-74
2475-79	2475-79
2480-84	2480-84
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2595-99	2595-99
2600-04	2600-04
2605-09	2605-09
2610-14	2610-14
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2625-29	2625-29
2630-34	2630-34
2635-3	

Eukaryota; N

Culicoides;

AUTHORS Genoscope.

JOURNAL Submitted (10/10/2010) 10:10:00

- Web : www.bce-berlin.de

AUTHORS	DATE
Roth, C.W., E	1960

JOURNAL, Submitted (1999)

COMMENT	THIS CLONE
	delivered

Laboratory c
Restaur

FEATURES

10/

$$\frac{d}{dt}$$

/cj

BASE COUNT	147 a
OPTICN	

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alignment_scores:
    Quality: 202.50      Length: 102
    Ratio: 2.664        Gaps: 2
    Percent Similarity: 74.510      Percent Identity: 45.098

alignment_block:
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Align seg 1/1 to reverse of: CNS0100L from: 1 to: 681

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|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
304 ACCCTGCTCAATTCCTTCACGTGCTACTACCCGACGCGCGCAAACTGTG 255
24 pAsnArgLeuArgAspAspAlaIleAsnLeuYssSerLysGlyIleTha 41
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
254 GGAAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 205
41 IaValIrpIleProProIaIrpLysGlyThrSerGlnAsn...AspVal 56
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204 ACCTGTGG.CTGGCGCGCTCAACAAAGGCGCGCTCCGCGCGCTCTCTCG 156

57 GlyTYrGlyAlaTyrAspLeuTyrAspLeuGlyGluIleAsnGlnLysG 73
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155 GCGTACGACTACTTACATCTGTCGATCTCGCGGAATTGACCGAAGAAG 106
73 YrhrIaIaTgTrrLysTyrGlyThrArgSerGlnLeuGlnGlyAlaValr 90
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
105 CAGCGTGGCGCACCAATACGCGCAGCAAGCGCGCGCTCGAACAGCTCGCG 56

90 hSerLeuLysAsnAsn..GlyIleGlnValTyrGlyAspValaIleMeta 106
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106 snHis 107
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5 ACCAC 1

seq_name: gb_gss:AQ159867

seq_documentation_block:
LOCUS AQ159867 694 bp DNA GSS 09-SEP-1998
DEFINITION mg9b0002G08r CUD1 Rice Blast BAC Library Magnaporthe grisea genomid
clone mgxb0002G08r, DNA sequence.
ACCESSION AQ159867
VERSION AQ159867.1 GI:3556856
KEYWORDS GSS.
SOURCE Magnaporthe grisea.
ORGANISM Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes; Incertae sedis; Magnaportheaceae; Magnaporthe.
1 (bases 1 to 694)
Yu,Y., Zhu,H., Boyd,C.A., Gaudette,B., Gayle,A., Kingsbury,R.,
Phillips,K., Sasinowski,M., Ming,R.A., and Dean,R.A.
A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
Genome
Unpublished (1998)
Contact: Dean RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson University, Clemson, SC 29634
Tel: 864 656 5737
Fax: 864 656 4293
Email: rdeane@clemson.edu
Seq primer: GGAACACAGCTATGACCATG
Class: BAC ends
High quality sequence stop: 452.

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	/strain="70-15"

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/risuc_type="Protoplasts"
/abd_host="E. coli DH10B"
/note="Vector: PACWICH; Site 1: HindIII; Site 2: HindIII;
Rice blast is one of the most devastating fungal diseases
of rice world wide. It is a filamentous ascomycete with
a haploid genome (n=7) of approximately 40 Mbp. Rice
blast is an important model fungal pathogen for studying
numerous aspects of the fungal-host interaction. In
order to facilitate genome wide analysis, a BAC library
containing 9316 clones with an average insert size of 130
kbp was constructed. This library represents greater
than 25X genome coverage. High density colony filters
are available upon request."

```

```

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US-09-590-375-2 x A0159867 ..

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360 .G|G|N|G|Y|T|P|R|S|E|V|A|P|H|E|T|Y|G|L|A|S|N|Y|T|Y|G|Y|.....I 374
|||||: ||||| ||||| ||||| ||||| ||||| |||||
200 TAAACAGCGACGACGCGTGGCTTCTTGGTGGACCTGTACGGACAGCGTGC 249
374 IePThrHnIsgLysValProSerMetLysSerLysIle.....AsPPro 388
|||||: ||||| ||||| ||||| ||||| ||||| |||||
250 TGGCGTGGCGGCGCGGCGCGCGCGCTGGCGGCGCTGTACGCGCGCG 299
389 LeuLeuGlnAlaArgGlnThrTyrAlaTyrGlyThrGlnHisAspTyrPh 405
|||||: ||||| ||||| ||||| ||||| ||||| |||||
300 CTGATGCTGGCGCGCAAGCTCTGGGGGTACGGCACCGAGCGGCGCTACT 349
405 e.....AsPnHisAspIleIeG|Y|T|P|H|A|T|G|L|S|N|Y|A|S|P|S 419
| |||||: ||||| ||||| ||||| ||||| ||||| |||||
350 TTGGCGGAGAGGGCGCGAGACGCTGCGCTTCCAGCGGCTTCCGCG... 395
419 eRSeHnIspPro.....AsnSerGlyLeuAlaThrIleMetSer 431
|||||: ||||| ||||| ||||| ||||| ||||| |||||
396 .....CACCCGCGCGCTCCGCGGCGGCGGCGCTGGCGCTCTCGGCCAC 440
432 AspGly...ProGlyGlnAsnLysTyrMetTyrValGlyLysHisLysAl 447
|||||: ||||| ||||| ||||| ||||| ||||| |||||
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447 aGlyGlnValTPrArgAspIleThrGlyAsnArgSerGlyThrValHnI 464
|||||: ||||| ||||| ||||| ||||| ||||| |||||
491 CGGGCAGGCGTGGACGACCTGCTCGGACCAAGTCTGGGCGTGGTGTGCG 540
464 IeAsnAlaAspG|Y|T|P|G|L|Y|A|S|N|P|H|E|T|Y|A|L|A|S|N|Y|L|A|V|A|L|S|E|R 480
|||||: ||||| ||||| ||||| ||||| ||||| |||||
541 TCGACCGCGCGGCTACGCGGAGTTTCCGTTCGTCCACGAGGCGGTACAC 590
481 ValTPrValLysGln 485
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591 GTTGGGTGTCACGAG 605

seq_name: gb_est2:B581061
seq_documentation_block:

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LOCUS      BG581061          558 bp      mRNA      EST
DEFINITION EST482791 GVN Medicago truncatula cDNA clone pgVN-63M12 5' end,
            mRNA sequence.
ACCESSION  BG581061
VERSION    BG581061.1  GI:13596125
KEYWORDS   EST.
SOURCE     barrel medic.
ORGANISM   Medicago truncatula
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eustosids I; Fabales; Fabaceae; Papilionoideae; Trifoliales;
            Medicago.
TITLE      1 (bases 1 to 558)
AUTHORS     Fedorova,M., Pearson,B.L., Samac,D.A., Vance,C.P., Gantt,G.S., Town
            ,C.D., Van Aken,S., Utechtack,T., Cho,J. and Fraser,C.M.
COMMENT    ESTs from one month old nitrogen-fixing root nodules of Medicago
            truncatula, 2001
JOURNAL    Unpublished (2001)
COMMENT    Contact: Carroll P. Vance
            Department of Agronomy and Plant Genetics
            University of Minnesota
            441 Borland Hall, 1991 Upper Buford Circle, St.Paul, MN 55108 USA
            Tel: 612 625 5715
            Fax: 651-649-5058
            Email: vance004@maroon.tc.umn.edu
            University of Minnesota name: M832117e TIGR sequence name:
            MTCDD78TK More information is available at: http://www.medicago.org
FEATURES   Seq primer: SKmod (CTA GAA CTA gfg gat CC).
SOURCE     Location/Qualifiers
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source
1. 358
/organism="Medicago truncatula"
/cultivar="genotype A17"
/db_xref="taxon:3880"
/clone="pGVN-63M12"
/clone_1lb="GVN"
/tissue_type="N2-fixing root nodules"
/dev_stage="effective root nodules harvested one month
post inoculation with Sinorhizobium meliloti"
/lab_host="E. coli strain XL04R"
/note="Vector: pBluescript SK-; site_1: EcoRI; site_2:
XhoI; cDNA was prepared from polyA+ enriched RNA from
effective root nodules harvested one month post
inoculation with Sinorhizobium meliloti. The cDNA was
directionally ligated into the uni-ZAP XR vector from
Stratagene and packaged using GigaPack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-ZAP phage using Ex-Assist
helper phage and propagated in XL04R cells."
169 a 110 c 115 g 163 t 1 others
BASE COUNT
ORIGIN

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alignment_scores:      Length: 230
                        Quality: 197.00
                        Ratio: 1.684
                        Gaps: 8
Percent Similarity:    50.870
Percent Identity:      26.522

alignment_block:
US-09-590-375-2 x BG581061 ..

Align seg 1/1 to: BG581061 from: 1 to: 558

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[illegible]

42 atrpIleProAlaITrpLysGlyThrSerClnAsnAspValGlyTyr 58
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125 TTGGCTCTCTCT.....CCATCTCAAGTGTGGTCTTCAAGATAT 168

59 g1a1a1yAspLeuTyRAspLeuGlyGluPheAsnGlnLysGlyThrVa 75
 169 CTCACGAGAAAGACTTATGATCTTGAT..... 195
 75 lArgThrLysTyRgLyThrArgSerGlnLeuGlnLysAlaValThrSerL 92
 196 .GCATCAAAATACGGTTCMAAAGATGACCTAAAGTCACTAAATTCAGAGCTT 244
 92 euLYsAsnAsnGlnLysIleGlnValTYRGLYAspValValMetAsnHisLys 108
 245 TCAGAGATTAAGAGATCAATGTTCTAGCTGACATGATGTCACCACT... 291
 109 G1yG1yAlaAspG1yThrG1uMetValAsnAlaValG1uValAsnArgSe 125
 292AGAAC 296
 125 rAsnArgAsnGlnGlnLysSerGlyGluTyThrIleGlnAlaThrPThrL 142
 297 AGCAGAAAGAAAGATGATAGAGCATCTATTCCTC..... 333
 142 ySPheAspPheProGlyArgGlyAsnThrHisSerAsnPheLysTrpArg 158
 334TTTGAAGGT...GGGACTCCTGATTCAAACTT..... 363
 159 TrpTyRHisPheAspGlyThrAspTrpAspGlnSerArgGlnLeuGlnAs 175
 364GATTGGGGCCCATCTTTCATTTCGCAAGA 392
 175 nLYsIleTyRlysPheArgGlyThrGlyLysAlaThrAspTrpGluVala 192
 393 TGACACCTGCTTATTCAGATGCACCTGA.....A 421
 192 SP1leGluAsnGlnLysAsnTyRAspTyRLeuMetTyRAlaAspIleAspMet 208
 422 ACCTGATATGGAGAG...GGCTATCAAGCTGCACCTGACATTCATCAT 468
 209 AspHisProGluValIleAsnGlnLeuArgAsnTrpGlyValTrpTyRTh 225
 469 CTCATTCCTCAAGTACAAAAGAGATTACTGATGATGATGATGATGCTCA 518
 225 rAsnThrLeuAsnLeuAspGlyPheArgIleAspAlaVal 238
 519 AACTGAAATGTGATTTCTGTGTGGAGATTGATTTTGTG 558
 seq_name: gb_est2:BF637944
 seq_documentation_block: 587 bp mRNA EST 19-DEC-2000
 LOCUS BF637944
 DEFINITION NF041C08PLF1056 Phosphate starved leaf Medicago truncatula cDNA
 clone NF041C08PL 5', mRNA sequence.
 ACCESSION BF637944
 VERSION BF637944.1 GI:11902102
 KEYWORDS EST.
 SOURCE
 ORGANISM
 .barrel medic.
 Medicago truncatula
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eustosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
 Medicago.
 1 (bases 1 to 587)
 REFERENCE
 AUTHORS Liu,J., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores
 H.R., Iman,J.T., Weller,J.W., May,G.D. and Harrison,M.J.
 TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation
 Medicago truncatula phosphate-starved leaf library
 JOURNAL Unpublished (2000)
 COMMENT
 Contact: Harrison MJ
 Plant Biology Division
 The Samuel Roberts Noble Foundation
 2510 Sam Noble Parkway, Ardmore, OK 73402, USA
 Tel: 580 221 7325
 Fax: 580 221 7380
 Email: mjharrison@noble.org

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 Plate: 041 row: C column: 08
 Seq primer: TCACAGGAAACAGCTATGAC.
 Location/Qualifiers
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 1. 587
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 /db_xref="taxon:3880"
 /clone="NF041C08PL"
 /clone_lib="Phosphate starved leaf"
 /tissue_type="leaf"
 /dev_stage="trifoliolate"
 /note="Vector: Lambda Zap; At the trifoliolate stage, M. truncatula plants were transplanted to phosphate-free sand and grown for a further 30 days. During this 30 day period, the plants were fertilized twice weekly with 1/2 Hoaglands solution containing only 20um potassium phosphate. RNA was prepared from above ground tissues."
 BASE COUNT 172 a 117 c 119 g 179 t
 ORIGIN
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 Quality: 196.00 Length: 228
 Ratio: 1.675 Gaps: 8
 Percent Similarity: 51.316 Percent Identity: 26.316
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 us-09-590-375-2 x BF637944 ..
 Align seg 1/1 to: BF637944 from: 1 to: 587
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 59 CTTCTTCAGGGAATCACTGCGAGTCAGTACAGTACAAAGAGATGGGTACAA 108
 25 nArgLeuArgAspAspAlaAlaAsnLeuLysSerLysGlyIleThrAlaVal 42
 109 CTTCTTGAAGAACCTCATCTCCGTGACCTAGCAAAATCTGGAAATACACATG 158
 42 aTrpIleProAlaTrpLysGlyThrSerGlnAsnAspAlaGlyTrp 58
 159 TTTGGCTTCCTCTCT....CCATCTCAAAAGTGTGGTCTTCAAGAGAT 202
 59 G1yAla1yAspLeuTyRAspLeuGlyGluPheAsnGlnLysGlyThrVa 75
 203 CTCACGAGAAAGACTTATGATCTTGAT..... 229
 75 lArgThrLysTyRgLyThrArgSerGlnLeuGlnLysAlaValThrSerL 92
 230 .GCATCAAAATACGGTTCMAAAGATGACCTAAAGTCACTAAATTCAGAGCTT 278
 92 euLYsAsnAsnGlnLysIleGlnValTYRGLYAspValValMetAsnHisLys 108
 279 TCAGAGATTAAGAGATCAATGTTCTAGCTGACATGATGTCACCACT... 325
 109 G1yG1yAlaAspG1yThrG1uMetValAsnAlaValG1uValAsnArgSe 125
 326AGAAC 330
 125 rAsnArgAsnGlnGlnLysSerGlyGluTyThrIleGlnAlaThrPThrL 142
 331 AGCAGAAAGAAAGATGATAGAGCATCTATTCCTC..... 367
 142 ySPheAspPheProGlyArgGlyAsnThrHisSerAsnPheLysTrpArg 158
 368TTTGAAGGT...GGGACTCCTGATTCAAACTT..... 397
 159 TrpTyRHisPheAspGlyThrAspTrpAspGlnSerArgGlnLeuGlnAs 175
 398GATTGGGGCCCATCTTTCATTTCGCAAGA 426
 175 nLYsIleTyRlysPheArgGlyThrGlyLysAlaThrAspTrpGluVala 192

AUTHORS Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Imman, J.T., Weller, J.W. and May, G.D.
TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation - Center for Medicago Genomics Research
JOURNAL Unpublished (2000)
COMMENT Contact: Dixon RA
 Plant Biology Division
 The Samuel Roberts Noble Foundation
 2510 Sam Noble Parkway, Ardmore, OK 73402, USA
 Tel: 580 221 7302
 Fax: 580 221 7380
 Email: radixon@noble.org
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 Seq primer: TCACACGGAAGACGCTATGAC.

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 /db_xref="taxon:3880"
 /clone="NF077E12RC"
 /clone_lib="Elicited cell culture"
 /tissue_type="Cell cultures derived from root tissues"
 /dev_stage="Cell suspensions were subcultured every 14 days. Cells were induced six days after subculture"
 /note="Vector: Lambda Zap; Cells were induced with yeast cell wall extracts equivalent to 50ug/ml glucose in the final concentration. Samples were taken at 0.5, 1, 12 and 24 hours after induction. Equal amounts of RNA from each time point were pooled and used for mRNA isolation."

BASE COUNT 183 a 129 c 125 g 197 t 1 others
ORIGIN

alignment_scores:
 Quality: 195.00 Length: 232
 Ratio: 1.681 Gaps: 8
 Percent similarity: 50.000 Percent identity: 26.724

alignment_block:
 US-09-590-375-2 x BF647599 ..

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95 TCGGAGCTCAAGTACAAAGAGGATGCTGCAACTCTTTCAAAACCTCAT 144
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31 aAlAsnLeuLysSerLysGlyIleThrAlaValTrpIleProAlaT 48
||||| ||| ||||| ||||| ||||| ||||| ||||| |||||
145 TCCTGACCTAGCAATGCTGGAATACATGTTGGCTTCCTCT... 190
||||| ||| ||||| ||||| ||||| ||||| ||||| |||||
48 rPLyGlyThrSerGlnAsnAspValGlyTyrGlyAlaTyrAspLeuTyr 64
||| ||| ||||| ||||| ||||| ||||| ||||| |||||
191 ..CCATCTCAAAAGTGTGCTCTCAAGGATATCTCCAGGAAGACTTAT 238
||||| ||| ||||| ||||| ||||| ||||| ||||| |||||
65 ASPLenGlyGluPheAsnGlnLysGlyThrValArgThrLysTyrGlyTh 81
||||| ||| ||||| ||||| ||||| ||||| ||||| |||||
239 GATCTTGAT.....GCATCAAAATACGGTTC 264
||||| ||| ||||| ||||| ||||| ||||| ||||| |||||
81 rARGSerGlnLeuGlnGlyAlaValThrSerLeuLysAsnAsnGlyIleG 98
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265 AAAAGATGCAAGTCAAGTCACTATTGCACTTCAAGATTAAGGATCA 314
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98 lInValTyrGlyAspValValMetAsnHisLysGlyAlaLaspGlyThr 114
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315 ATTGCTTACTGATAGTATGATCAACCAT..... 343
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115 GluMetValAsnAlaValGluValAsnArgSerAsnArgAsnGlnGlu 131
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344 .....AGACAGCAGGAAGAAAGAGATCA 366
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131 eSerGlyGlyTyrThrIleGluAlaTrpThrLysPheAspPheProGly 148
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367 TAGAGCATCTATTCCTC.....TTGAGGT. 394
148 rGGLysnThrHisSerAsnPhelySTPArgTyrThrHisPheSpLy 164
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165 ThrASPTrpAspGlnSerArgGlnLeuGlnAsnLysIleTyrLysPheAr 181
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416 ..GATGGGGCCCATCTTTCATTGCAAGATGACACGCTATTATTCAGA 462
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463 TGGCACTGA.....AACCTGATGACGAGAG. 490
198 YrASPtyrLeuMetYrAlaAspIleAspMetAspHisPheProGluVal 214
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491 ..GGCTATCAAGCTGCACCTGACATTGATCATCTCAACTCAATACAA 538
||||| ||| ||||| ||||| ||||| ||||| ||||| |||||
215 AsnGluLeuArgAsnTrpGlyValTrpYrThrAsnThrLeuAsnLeuAs 231
||||| ||| ||||| ||||| ||||| ||||| ||||| |||||
539 AAAGATTTATCTGATGATGATGATGATGATGATGATGATGATGATGAT 588
||||| ||| ||||| ||||| ||||| ||||| ||||| |||||
231 pGlyPheArgIleAspAlaValLysHisIleLysTyrSerTyrThr 246
||||| ||| ||||| ||||| ||||| ||||| ||||| |||||
589 TCGTTGAGATTTGATTTTTCAAANGTATGCGCTACCATATACA 634
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seq_name: gb_est2:BF011027

seq_documentation_block:

LOCUS BF011027 771 bp mRNA EST 06-OCT-2000
DEFINITION SB233 Sugar Beet germination cDNA library Beta vulgaris cDNA clone YS016f79.5' similar to alpha amylase, mRNA sequence.
ACCESSION BF011027
VERSION BF011027.1 GI:10711301
KEYWORDS EST.
SOURCE Beta vulgaris.
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae; Caryophyllales; Chenopodiaceae; Beta.

REFERENCE
 1 (bases 1 to 771)
 de los Reyes, B.G., McGrath, J.M., Myers, S. and Derrico, C.
 Differential gene expression in sugar beet seedlings (Beta vulgaris) germinated under stress conditions
 Unpublished (2000)
 Contact: J. Mitchell McGrath
 Sugar Beet Genetics Lab., USDA/ARS/Sugar Beet and Bean Research Unit
 Michigan State University
 494 Plant and Soil Sci. Bldg., East Lansing MI 48824, USA
 Tel: (517)-432-2355
 Fax: (517)-337-6782
 Email: milchmge@pilot.msu.edu
 Seq primer: T3
 High quality sequence stop: 750.

FEATURES
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1..771
 Location/Qualifiers
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 /cultivar="USH20"
 /db_xref="taxon:161934"
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 /clone_lib="Sugar Beet germination cDNA library"
 /tissue_type="whole seedlings"
 /dev_stage="4-day germination under stress (salt/NaCl, denaturation/Mannitol and anaerobic stress)"
 /lab_host="SOLR"
 /note="Organ: seeds; Vector: pBluescript II KS (+) excised from Lambda Uni-Zap XR; Site:1: EcoRI; Site:2: XhoI; cDNAs were derived from reverse transcription of pooled mRNA samples from stressed seedlings (germinated for 4 days in 150mM NaCl, 200mM Mannitol, submerged in distilled water and 0.3% Hydrogen peroxide). The cDNA library was generated by directional ligation of the cDNAs in the


```

6  AaagclgYhmetetglnYtrpneGlntrPhnIsleuProAsnspRglYas 22
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
373 AACGAGACGCTCTTTCAAGCGCTTTGATGGCCACCTCCCGCCAGCAAGCG 422
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
22  nhIstrPAsnArgLeuArspAspAspAlaAlaAsnLeuLysSerLysGlyI 39
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
423 TCACGTGGCGTCGACTCATCTCATCTCATACCCACGCTTGCCTTTGGGCA 472
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
39  lethAlaValATrPleProAlaTrPlysgLYthrSer..... 52
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
473 TCACCAAGCTTTGGATCCCAACGGCGCTGCAGAGGGCGGGGTGGCTGG 522
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
53  GlnAsnAspValGlyTrGlyAlaTrYAspLeuTrYAspLeuGlyLuph 69
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
523 AGCCAA.....GGCTAAGCAGCTTACGATCTGTATGATGTGGGCAgTT 566
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
69  eaSngInLysGlyThrValArg.....ThrLysTyrGlyTP 81
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
567 TGACACCAAGGCGCTCCAGNCGCAGCCAACTGGCCCCCAGACCCGAACTGGAC 616
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
81  htrArgSerGlnLeuGlnGlyAlaValThrSerLeuLysAsnAsnGlyIle 97
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
617 GAGCTCGTCCGCGCGCGGGGGGAGCGCGCA.....TTT 651
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
98  GlnValTrGlyAspValAlaMetAsnHisLysGlyGly 110
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
552 GAGATCCGTGTTAATGCCCTGTGAACACAGAGGCGCGG 690
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seq_name:	gb_est2:BI073204
seq_documentation_block:	
LOCUS	BI073204
DEFINITION	702 bp mRNA
	EST
	19-JUN-2001
	PIR2B_G10 Sugar Beet germination cDNA library Beta vulgaris cDNA 5'
	similar to alpha amylase, mRNA sequence.

ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllidae; Caryophyllales; Chenopodiaceae; Beta.

REFERENCE	AUTHORS	TITLE
1 (bases 1 to 702)	de los Reyes, B.G., McGrath, J.M. and Myers, S.	Differential gene expression in sugar beet seedlings (<i>Beta vulgaris</i>)

JOURNAL Unpublished (2001)
COMMENT Contact: J. Mitchell McGrath

Michigan State University
404 Plant and Soil Sci. Bldg., East Lansing MI 48824, USA
Tel: (517)-432-2355
Fax: (517)-337-6782
Email: mitchmcg@pilot.msu.edu
Seq primer: T3.

FEATURES	Location/Qualifiers
source	1. .702

1. 702
/organism="Beta vulgaris"
/cultivar="USH20"
/db_xref="taxon:161934"
/clone_id="Sugar Beet germination cDNA library"
/tissue_type="whole seedlings"
/dev_stage="4-day germination under stress (salt/NaCl,
dehydration/Mannitol and anaerobic stress)"
/lab_host="SOLR"
/note="Organ: seeds; Vector: pBluescript II KS (+) excised
from Lambda Uni-Zap XR; Site.1: EcoRI; Site.2: XhoI; cDNA
were derived from reverse transcription of pooled mRNA
samples from stressed seedlings (germinated for 4 days in
150mM NaCl, 200mM Mannitol), submerged in distilled water
and 0.3% Hydrogen peroxide). The cDNA library was

generated by directional ligation of the cDNAs in the EcoRI and XhoI sites of lambda uni-zap XR vector (Stratagene). The library was excised as a pluscript plasmid from lambda uni-zap XR by Exassist helper phage and plated on SOLR host cells.

BASE COUNT	205 a	128 c	167 g	201 t	1 others
ORIGIN					

alignment_scores:	quality:	181.50	length:	247
	ratio:	1.525	gaps:	9
Percent Similarity:	48.178	Percent Identity:	25.506	
alignment_block:	US-09-590-375-2 x BI073204	..		

Align seg 1/1 to: BI073204 from: 1 to: 702

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24 pAsnArghLeuArGAspAspAlaAlaAsnLeuLysSerLysGlyIleThra 41
163 TAATTCACAGAAACCACTCAATGCATGATGATTGGCTAGAGCAGGGCTTACAC 212
41 lAvalTrrIleProFroAlaTrrPlysGlyThrSerGlnAsnAspValGly 57
213 ATGTTTGGCTTCCTCCACCAACATCAATCGGTTTCTCTCAAA.....GGA 256
58 TyrGlyAlaTyrAspLeuTyrAspLeuGlyGlnPheAsnGlnLysGlyTh 74
257 TATCTTCCTGCAAGATTCGATATCATCTGAT..... 286
74 rValArghTrhLysTyrGlyThrArgSerGlnLeuGlnGlyAlaValThrs 91
287 ....GCATCTAGATrATGGCAACGGGGCTGATTTTAAAGACCTTGATTACG 332
91 eRLeuLysAsnAsnGlyIleGlnValTyrGlyAspValValMetAsnHis 107
333 CCTTCACCAACAAAAGCATCAATGCTGGCGATATAGTAAATTCAT 382
108 LysGlyGlyAlaAspGlyThrcIuMetValAsnAlaValGluValAsnAr 124
383 .....AG 384
124 gSerAsnArGAsnGlnGluIleSerGlyGluTrrThrIleGluAlaTrrP 141
385 ATGGCCAGATAAAGCAAGATGGTAGAGGAATCTATTGTATA..... 424
141 hrLysPheAspPheProGlyArgGlyAsnThrHisSerAsnPhelyStr 157
425 .....TTTAGAGT...GGAACTCCAGACGATCGCCCTAAGATTGG 460
158 ArgTrrTyrHisPheAspGlyThraSptrPAspGlnSerArgGlnLeuG 174
461 .....GGGCATGGGCTATTGGACAGGAT..... 484
174 nAsnLysIleTyrLysPheArgGlyThrcLysAlaTrrPAspTrrGluV 191
485 .....GACACTCAAT 494
191 aAspIleGluAsnGlyAsnTyrAsp.....TyrIuMetTyr 203
495 ACTCTGACGGTAGTGAATCTTAGACACTGGAAGCTACTGTTAGGTGTGCA 544
204 AlaAspIleAspMetAspHisPProGluValIleAsnGlnLeuArGAsnTr 220
545 CCGCATATAGACCACTTAATCCAAAGGCTACAAAGAGAACTACTGTATTG 594
220 pGlyValATrrPTrhAsnThrLeuAsnLeuAspGlyPheArgIleAspA 237

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/clone="c1EN12E8"
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/note="Vector: pBluescript SK(-); Site.1: EcoRI; Site.2:
XhoI; Supplier: Giovannoni; Fruit were tagged at the
breaker stage (first sign of lycopen accumulation on the
blossom end of the fruit) and harvested 7 days
post-breaker (fully red-ripe), 10 days post breaker, and
20 days post-breaker (over-ripe). 20 day fruit which
showed external or internal signs of pathogenesis were
discarded. Fruit were cut in half and the seeds and
locules were discarded prior to freezing the pericarp."

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ORIGIN

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US-09-590-375-2 x AW223546 ..

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Align seg 1/1 to: AW223546 from: 1 to: 678

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2 AACATTGATCATTCCTCCAGGAATTCGTGAAGAAGATATCATCGGAATGCTT 51
221 yAlaTrpTrpThrAsnThrLeuAsnLeuAspLysPheArgLysAlaVal 238
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52 ACTGCGCTGAGGAGAGAGATTGTTATGATGATGAGAGCGCTTGATTTTG 101
238 aLlyuHnIleLysTyrSerTyrThrArgAspTrpLeuThrHisValArg 254
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102 TTCGGGGGTTGGGGGTGTTATGTCGAAGATTACTG..... 139
255 AsnThrThrGlyLysPheMetPheAlaValAlaGluPheTrpLysAsn.. 270
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140 ..GAAGCAACTGAACCTTACTTCGCTGACGCGAGTTTGGGATTCCT 186
271 .....AspleuAla 274
187 CGTTATACTTATGAGAGATGATCACAATGACAAGATGCGCATAGGCGAGA 236
274 laIleGluAsnTyrLeuAsnLysThrSerTrpAsnHisSerValPheAsp 290
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237 GAATTAATGACAGTGAATGCTACTAATGAGAACTGCAAGACATTTGAC 286
291 ValProLeuHisTyrAsnLeuTyrAsnAlaSerAsnSerGlyTyrPhe 307
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287 GTGACACAGCAAGGAAATCTCTCATCTGCAATTCGAGATGTGAATACAG 336
307 e.....AspmetaArgAsnIleLeuAsnGlySerValAlaGlnLysH 321
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337 GCGACTATCCGATCCAGAAAGGGAACCTCCCGC...GTTGTTGATGGT 383
321 lSProlleHisAlaValThrPheValAspAsnHisAspSerGlnPheArg 337
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384 GGCACATCCGCTGCTTACATTATAGAAATCATGATCAGGTTCTACA 433
338 GluAlaLeuGluSerPheValGlnSerTrpPheLysPro..... 350
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434 CAGGCT.....CATTCGACATTTCCGTGGTGGGAAAGA 465
351 ...LeuAlaTyrAlaLeuIleLeuThrArgGlnGlnGlyTyrProSerV 366
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466 GATGCAAGGATATGCTATATCTGACT...CACCCGTGAGACCCGCTAG 512

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366 alphaPheTyrGlyAspTyrTyrGlyIleProThrHisGlyValProSerMet 382
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513 TCTTCTTT.....GATCACAATTTCTCTCTGTTAC 541
383 LysSerLysIleAspProLeuLeuGlnAlaArgGln 394
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seq_name: gb_gss:CNS0001B

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seq_documentation_block:

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DEFINITION Arabidopsis thaliana genome survey sequence SP6 end of BAC T7A19 of
TAMU library from strain Columbia of Arabidopsis thaliana, genomic
survey sequence.

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ACCESSION  AL091025
VERSION     AL091025.1 GI:5292179
KEYWORDS   GSS.
SOURCE     Arabidopsis thaliana
ORGANISM   thale cress.

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REFERENCE  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

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AUTHORS    1 (bases 1 to 456)
            Salanoubat,M., Choise,N., Artiguenave,F., Brothier,P., Wincker,P.,
            Samson,D., Saurin,W., Weissenbach,J. and Quetier,F.

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JOURNAL    Unpublished
REFERENCE  2 (bases 1 to 456)
            Genoscope.
            Direct Submission
            Submitted (25-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)

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FEATURES

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BASE COUNT      128 a      112 c      88 g      128 t
ORIGIN

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alignment_scores:
  Quality: 173.50      Length: 66
  Ratio: 3.402      Gaps: 1
  Percent Similarity: 77.273      Percent Identity: 48.485

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alignment_block:
US-09-590-375-2 x CNS0001B ..

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Align seg 1/1 to: CNS0001B from: 1 to: 456

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6 AsnglyThmMetMetGlnTyrPheGluTyrPheLysLeuProAsnAspLys 22
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
259 AACCTCACACCTCTTCAATCTTCAATCTTCAATCTTCAATCTTCAATCTT 308
22 nHisTrpAsnArgLeuAlaArgAspAlaAlaAsnLeuLysSerLysGlyI 39
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
309 TCTTGGTTACATGCGTGCATTAAGCAAAAGAACTGCGATCGATGGGGA 358
39 leThrAlaValTrpIleProAlaTrpLysGlyThr...SerGlnAsn 54
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
359 TTACCCATTTTGGCTCCACCGGCTTATAGTCAAGCCCTTGGCACAGAG 408
55 AspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuGlyGluPheAsn 70
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
409 GAGCCCGGTTATGCTGTATATGACCTGTACGATCTGGGGAATTTGAT 456
seq_name: gb_estl:AW709933

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seq_documentation_block: 436 bp mRNA EST 25-APR-2000
 LOCUS AW709933 d9b06ne.f1 Neurospora crassa evening cDNA library Neurospora crassa
 DEFINITION d9b06ne.f1 Neurospora crassa evening cDNA library Neurospora crassa
 CDNA clone d9b06ne 5', mRNA sequence.
 ACCESSION AW709933
 VERSION AW709933.1 GI:7599010
 KEYWORDS EST.
 SOURCE Neurospora crassa.
 ORGANISM Neurospora crassa.
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Sordariales; Sordariaceae; Neurospora.
 REFERENCE 1 (bases 1 to 436)
 AUTHORS Zhu, H., Lai, H., Kupfer, D., Dunlap, J.C. and Roe, B.A.
 TITLE Two Neurospora crassa EST databases
 JOURNAL Unpublished (1998)
 COMMENT Other_ESTS: d9b06ne.r1
 Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
 Department of Chemistry and Biochemistry
 Advanced Center for Genome Technology, University of Oklahoma
 620 Parrington Oval, Norman, OK 73019, USA
 Tel: 405 325 4912
 Fax: 405 325 7762
 Email: broe@ou.edu
 We anticipate the future release of the cDNA clones to the Fungal
 Genetics Stock Center
 Seq primer: Universal Forward Primer
 High quality sequence stop: 424.
 Location/Qualifiers

FEATURES
 source 1..436
 /organism="Neurospora crassa"
 /strain="Strain 30-7 (bd; A)"
 /db_xref="taxon:5141"
 /clone="d9b06ne"
 /clone_id="Neurospora crassa evening cDNA library"
 /tissue_type="tissue harvested following 22hr growth in
 dark"
 /note="Vector: pBluescript SK-; Site_1: XbaI; Site_2:
 EcoRI; See: Bell-Pedersen, D., et al. PNAS 93:13096,1996.
 5' end of cDNA cloned into XbaI site of pBluescript; 3'
 end of cDNA cloned into EcoRI site of pBluescript"

BASE COUNT 82 a 159 c 93 g 102 t
 ORIGIN

alignment_scores: Quality: 169.00 Length: 145
 Ratio: 2.036 Gaps: 4
 Percent Similarity: 57.241 Percent Identity: 31.034

alignment_block:
 US-09-590-375-2 x AW709933 ..

Align seg 1/1 to: AW709933 from: 1 to: 436

```

243 TyISerTyrThrArgAspTrpLeuThHisVal.....Ar 254
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2 TACTCTTGTGCGCGAATTTCTAGCCACATCGACCGCAGTGGCTCC 51
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
254 gAsnThrThiGlyLysPro.....MetPheAlaValAlaGluPheTrpL 269
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
52 TGGACCCCTGGAGCCCGAGGAGCTGTCATCGTGGCGCAATATCGGC 101
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
269 ySAsnAspLeuAlaAlaIleGluAsnTyrLeuAsnLysThrSerTrpAsn 285
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
102 GCGAAGATTCGAGTTCTCGCGGTACATCGAATTTATGACACCGCGC 151
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
286 HisSerValPheAspValProLeuHisTyrAsnLeu..... 297
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
152 TTGTCTCTTCGACGTGCAATTAAGTCTCAACTTCTCCCGCATCTTT 201
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
298 .....TyrAsnAlaSerAsnSerGlyLy..... 305
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
202 AGCTTCGACACACCTCCAAAGCCTCTCCACCGGTGAGTGAGTGGCTC 251

```

```

306 .....TyrPheAspMetArgAsnIleLeuAsn 314
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
252 CCGGATCAGTACGAGCGACCGCGACACCGACCTCCGACCTTATTCGAC 301
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
315 GlySerValValGlnLysHisProIleHisAlaValThrPheValAspAs 331
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
302 GACACCTCTGCATCTGGAACCGCACAAACGCGCTCTCTGTGCTTAA 351
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
331 nHisAspSerGlnProGlyGluAlaLeuGluSerPheValGlnSerTrp 348
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
352 CCACGACACACAAAGGCGCAATCGCTCGAAACGCCCATAGGCCCTTCT 401
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
348 helysProLeuAlaTyrAlaLeuIleLeuThrArg 359
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402 TCATGCCCTCGCCTATTCGCTCATCTTACTTCGC 436

```

QY 6 NCTMAYEFEMHLPNDGNHNNRLDDAANLKSKITAVWIPAMKGTSONDVGAYADLYD 65
 DB 33 NCTLMQYEFEMWYRNDGNHNNRLDDAANLKSKITAVWIPAMKGTSONDVGAYADLYD 92
 QY 66 LGEFNOKGTVPKRYKTSRLOLGAVTSLKNNGIQYTGVDVYNNHKGADGTEYNAVEVNS 125
 DB 93 LGEFNOKGTVPKRYKTSRLOLGAVTSLKNNGIQYTGVDVYNNHKGADGTEYNAVEVNS 152
 QY 126 NNNOESGTYTEAMTKKDEPGRGNMHSNEKRWYHFDGTMDOSROJNKRYKRGCK 185
 DB 133 DNKNRISGEHRKAWTHFRPGSGSTYSDFKWMYHFDGTMDOSROJNKRYKRGCK 209
 QY 186 AMDWEVDIENGNYDYLMADIDMDPEVYNELRNNGVYNTNLTNDGERIDAVKIKKSY 245
 DB 210 AMDWEVDIENGNYDYLMADIDMDPEVYNELRNNGVYNTNLTNDGERIDAVKIKKSY 269
 QY 246 TRDMITLHVANTGKPMFAVEFKAIDLAIENYLNKTSNNHSEFVPLHYNLVYNSNGG 305
 DB 270 LRDVYNNHREKTKEMFVYAEYQMDLGALENYLNKTNENHSEFVPLHYNFAASTOGG 329
 QY 306 YEDMNNIUNGSVYOKHPIHAYFVNNDHSDGSEALESPVOSFEPKPLAVALITREOGYPS 365
 DB 330 GIDMKRLSLSTVSKHPLAATFVDNHDTPGOSLESTVOTWFKPLAVALITREOGYPS 389
 QY 366 VYEGDYGIPTG-----VPSMKRIDPLLAQOTVAYGTOHDYFDHDIIGTREGSPS 420
 DB 390 VYEGDYGIPTG-----VPSMKRIDPLLAQOTVAYGTOHDYFDHDIIGTREGSPS 447
 QY 421 HNSGLATITMSDPCGKNNKMYGKHKAGVMDITGNSGTVTINADGNGFTVNGAYS 480
 DB 448 VANSGLAALITDPCGAKRMVYGRONAGETWHDITGNRSEPVYINSEGEFHVNGSVS 507
 QY 481 VWVK 485
 DB 508 IYVOR 512

RESULT 3
 AMY_BACST STANDARD: PRT: 549 AA.

AC P06279; 045519; (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 33, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE ALPHA-AMYLASE PRECURSOR (EC 3.2.1.1) (1,4-ALPHA-D-GLUCAN
 GLUCANOHYDROLASE).
 GN AMYS.
 OS Bacillus stearothermophilus.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Geobacillus.
 OX NCBI_TaxID=1422;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 35-39.
 RA MEDLINE=85234394; PubMed=3924897;
 RA Nakajima R., Imanaka T., Alba S.;
 RT "Nucleotide sequence of the Bacillus stearothermophilus alpha-amylase
 gene.";
 RT J. Bacteriol. 163:401-406(1985).
 RN [2]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC STRAIN=DY5/PH1300;
 RX MEDLINE=86008166; PubMed=3876333;
 RX Ihara H., Sasaki T., Tsuboi A., Yamagata H., Tsukagoshi N., Uda S.;
 RT "Complete nucleotide sequence of a thermophilic alpha-amylase gene:
 RT homology between prokaryotic and eukaryotic alpha-amylases at the
 RT active sites.";
 RT J. Biochem. 96:95-103(1985).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NZ-3;
 RX MEDLINE=86195857; PubMed=3009417;
 RX Gray G.L., Mainzer S.E., Rey M.W., Lamsa M.H., Kindle K.L.,
 RA Carmona C., Requadt C.;

RT "Structural genes encoding the thermophilic alpha-amylases of
 RT Bacillus stearothermophilus and Bacillus licheniformis.";
 RT J. Bacteriol. 166:635-643(1986).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Suominen I., Karp M., Lautamo J., Knowles J., Mantsaelae P.;
 RT "Thermotable alpha amylase of Bacillus stearothermophilus: cloning,
 RT expression, and secretion by Escherichia coli.";
 RT (In) Chaloupka J., Krumphanzl V. (eds.);
 RL Extracellular enzymes of microorganisms, pp.129-137, Plenum Press,
 RL New York (1987).
 RN [5]
 RP SEQUENCE OF 1-122 FROM N.A., AND SEQUENCE OF 35-48.
 RC STRAIN=DY-5;
 RX MEDLINE=86059211; PubMed=2999073;
 RX Tsukagoshi N., Iritani S., Sasaki T., Takemura T., Ihara H.,
 RA Ideta Y., Yamagata H., Uda S.;
 RT "Efficient synthesis and secretion of a thermophilic alpha-amylase by
 RT protein-producing Bacillus brevis 47 carrying the Bacillus
 RT stearothermophilus amylase gene.";
 RT J. Bacteriol. 164:1182-1187(1985).
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-ALPHA-GLUCOSIDIC
 CC LINKAGES IN OLIGOSACCHARIDES AND POLYSACCHARIDES.
 CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
 CC KNOWN AS THE ALPHA-AMYLASE FAMILY.
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 CC
 DR EMBL, M11450; AAA22235.2; -
 DR EMBL, X02769; CAA26547.1; -
 DR EMBL, M57457; CAA22227.1; -
 DR EMBL, M13255; AAA22241.1; -
 DR PIR, A00845; ALBSF.
 DR PIR, A24549; A24549.
 DR HSSP, P06278; 1BPL.
 DR InterPro, IPR000461; Alpha-amylase.
 DR Pfam, PF00128; alpha-amylase; 1.
 KW Hydrolyase; Glycosidase; Carbohydrate metabolism; Signal.
 FT SIGNAL 1 34
 FT CHAIN 35 549
 FT ACT_SITE 268 268
 FT ACT_SITE 272 272
 FT ACT_SITE 365 365
 FT CONFLICT 13 13
 FT CONFLICT 19 19
 FT CONFLICT 23 23
 FT CONFLICT 31 31
 FT CONFLICT 107 107
 FT CONFLICT 167 167
 FT CONFLICT 179 179
 FT CONFLICT 251 251
 FT CONFLICT 260 260
 FT CONFLICT 284 284
 FT CONFLICT 312 312
 FT CONFLICT 338 338
 FT CONFLICT 342 342
 FT CONFLICT 346 346
 FT CONFLICT 376 376
 FT CONFLICT 526 526
 FT CONFLICT 527 527
 FT CONFLICT 535 535
 SQ SEQUENCE 549 AA; 62670 MM; 3A2DD93A955E79D3 CRC64;

Query Match 69.8%; Score 1894.5; Dbl 1; Length 549;
 Best Local Similarity 68.4%; Pred. No. 6.3e-122;
 Matches 327; Conservative 70; Mismatches 80; Indels 1; Gaps 1;

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 28, 2001, 17:03:57 ; Search time 18.04 Seconds

(without alignments)
985.723 Million cell updates/sec

Title: us-09-590-375-2
Perfect score: 2713
Sequence: 1 HHNGTNGTMMQYFEMHLPND.....ADGNGFTVNGAVSWVKQ 485

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 3664827 residues
Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2410	88.8	518	1 AMT6_BACS7	P19571 bacillus sp
2	1906	70.3	512	1 AMY_BACLT	P06278 bacillus li
3	1894.5	69.8	549	1 AMY_BACST	P06279 bacillus st
4	1843	67.9	514	1 AMY_BACAM	P00692 bacillus am
5	1053	38.8	494	1 AMY2_SALTY	P26613 salmonella
6	1022	37.7	495	1 AMY2_ECOLI	P26612 escherichia
7	315	11.6	1196	1 AMYB_PABPO	P21543 paenibacilli
8	294	10.8	440	1 AMY3A_ORYSA	P27932 oryza sativ
9	287.5	10.6	421	1 AMY4_VIGMU	P17859 vigna mungo
10	284.5	10.5	548	1 AMT4_PSEST	P13507 pseudomonas
11	283.5	10.4	551	1 AMT4_PSESA	P22963 pseudomonas
12	281	10.4	713	1 AMYR_BACS8	P17692 bacillus sp
13	277	10.2	713	1 CBGT_BACS0	P06612 bacillus sp
14	275	10.1	712	1 CBGT_BACS3	P09121 bacillus sp
15	274.5	10.1	718	1 CBGT_BACCI	P30920 bacillus ci
16	271	10.0	713	1 CBGT_BACCI	P43379 bacillus ci
17	270	10.0	713	1 CBGT_BACSP	P30921 bacillus sp
18	269.5	9.9	718	1 CBGT_BACSS	P31747 bacillus sp
19	266.5	9.8	435	1 AM3D_ORYSA	P27933 oryza sativ
20	265	9.8	437	1 AM3B_ORYSA	P27937 oryza sativ
21	264	9.7	427	1 AMY2_ORYSA	P27939 oryza sativ
22	263.5	9.7	427	1 AMY2_ORYSA	P04063 hordeum vul
23	261.5	9.6	710	1 CBGT_THETU	P26827 thermoaer
24	261	9.6	429	1 AMY6_HORVU	P04750 hordeum vul
25	260.5	9.6	428	1 AMY1_ORYSA	P17654 oryza sativ
26	260	9.6	368	1 AMY3_HORVU	P04747 hordeum vul
27	260	9.6	438	1 AMY1_BACCI	P08137 bacillus ci
28	259.5	9.6	528	1 AMY1_HORVU	P00693 hordeum vul
29	255.5	9.4	718	1 CBGT_BACLI	P14014 bacillus li
30	253	9.3	703	1 CBGT_BACS2	P31746 bacillus sp
31	249.5	9.2	413	1 AMY3_WHEAT	P08117 triticum ae
32	247.5	9.1	711	1 CBGT_BACST	P27997 bacillus st
33	246	9.1	437	1 AM3E_ORYSA	P27934 oryza sativ

34	243	9.0	713	1 CDG2_PAEWA	P31835 paenibacilli
35	237.5	8.8	498	1 AMYB_ASPPW	P002905 aspergillus
36	237.5	8.8	499	1 AMYB_ASPPW	P002906 aspergillus
37	236.5	8.7	443	1 AM2A_ORYSA	P27935 oryza sativ
38	233.5	8.6	499	1 AMY2_ASPPOR	P10529 aspergillus
39	232.5	8.6	445	1 AMY2_ORYSA	P27941 oryza sativ
40	231	8.5	717	1 AMYB_BACST	P19531 bacillus st
41	230.5	8.5	499	1 AMYB_ASPPH	P30292 aspergillus
42	225	8.3	714	1 CDG1_PAEWA	P04830 paenibacilli
43	223.5	8.2	441	1 MGT4_THENA	P80099 thermotoga
44	222	8.2	442	1 MGT4_THENA	P80099 thermotoga
45	219	8.1	494	1 AMY1_SACPI	P21567 saccharomyce

ALIGNMENTS

RESULT ID	AMT6_BACS7	STANDARD:	PRT:	518 AA.
AC	P19571:			
DT	01-FEB-1991 (Rel. 17, Created)			
DT	01-FEB-1991 (Rel. 17, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	GLUCAN 1,4-ALPHA-MALTOHEXAOSIDASE PRECURSOR (EC 3.2.1.98) (66-AMYLASE)			
DE	(MALTOHEXAOSIDE-PRODUCING AMYLASE) (EXO-MALTOHEXAOMYDROLASE).			
OS	Bacillus sp. (strain 707).			
OC	Bacteria; Firmicutes; Bacillus/Clostridium group;			
OC	Bacillus/Staphylococcus group; Bacillus.			
OX	NCBI_TaxID=1416;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 34-36.			
RX	MEDLINE=88162814; PubMed=3258152;			
RA	Tsukamoto A., Kimura K., Ishii Y., Takano T., Yamane K.;			
RT	Nucleotide sequence of the maltotetraose-producing amylase gene from			
RT	an alkaliphilic Bacillus sp. #707 and structural similarity to			
RT	liquefying type alpha-amylases.";			
RL	Biochem. Biophys. Res. Commun. 151:25-31(1988).			
CC	-1- CATALYTIC ACTIVITY: HYDROLYSIS OF 1,4-ALPHA-D-GLUCOSIDIC LINKAGES			
CC	IN AMYLACROUS POLYSACCHARIDES SO AS TO REMOVE SUCCESSIVE			
CC	MALTOHEXAOSIDE RESIDUES FROM THE NON-REDUCING CHAIN ENDS.			
CC	-1- PATHWAY: DEGRADATION OF STARCH.			
CC	-1- SUBCELLULAR LOCATION: SECRETED.			
CC	-1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO			
CC	KNOWN AS THE ALPHA-AMYLASE FAMILY.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	entities requires a license agreement (see http://www.isb-sdb.ch/announce/			
CC	or send an email to license@sdb.ch).			
CC	-----			
DR	EMBL, M18862; AAA2231.1; -			
DR	PIR; A27705; A27705.			
DR	HSSP; P06278; 1BPL.			
DR	InterPro; IPR000461; Alpha.amylase.			
DR	PIfam; PF00128; alpha-amylase; 1.			
KW	Hydrolase; Glycosidase; Carbohydrate metabolism; Signal.			
FT	SIGNAL			
FT	CHAIN 1 33			
SO	SEQUENCE 518 AA; 59009 MW; 3A61E21612682C4 CRC64;			

Query Match 88.8%; Score 2410; DB 1; Length 518;
Best Local Similarity 86.4%; Pred. No. 4.7e-157;
Matches 419; Conservative 36; Mismatches 10; Indels 0; Gaps 0;

QY 1 HHNGTNGTMMQYFEMHLPNDGHHNRLRDDANLKSITAVWIPAWKGTSONDVGCA 60
DB 34 HHNGTNGTMMQYFEMHLPNDGHHNRLNSDASNLKSGITAVWIPAWKGTSONDVGCA 93

OY 61 YDIYDLGEFNQKGVNRTKYGTSRLOCAVTSKNNCIQYGGVYVNNHKGADGTEWNAV 120
 DB 94 YDIYDLGEFNQKGVNRTKYGTSRLOCAVTSKNNCIQYGGVYVNNHKGADGTEWNAV 153
 OY 121 EVNRSNNQELSGEYVTEAVTKFDFGPGRTGHSNFKRWYHFDGTDMDOSROLQNKYKF 180
 DB 154 EVNRSNNQELSGEYVTEAVTKFDFGPGRTGHSNFKRWYHFDGTDMDOSROLQNKYKF 213
 OY 181 RGTGKAMDWEVDLENGVYDYLMTADIDMDHPEYINELRNKGVYTNLTNIGRIDAVKH 240
 DB 214 RGHKAKAMDWEVDLENGVYDYLMTADIDMDHPEYINELRNKGVYTNLTNIGRIDAVKH 273
 OY 241 IKYSTRTDLTHVNTGKRPMEFAVEFMKNDLAIENYLNKTSNHSVEVDPLHYLYNA 300
 DB 274 IKYSTRTDLTHVNTGKRPMEFAVEFMKNDLAIENYLNKTSNHSVEVDPLHYLYNA 333
 OY 301 SNSGCFPMRNILNGSVYOKHPIHAYTFVDNHDSPGEALESEVOSFVKPLATLITRE 360
 DB 334 SKSGNMYMRNIFNCTVYGRHPSHAYTFVDNHDSPGEALESEVOSFVKPLATLITRE 393
 OY 361 OGYSVFTGYGIPTHGVPSMKSKIDPLAQRQYVAGTQHDYFHHDIIGWTRGSS 420
 DB 394 OGYSVFTGYGIPTHGVPSMKSKIDPLAQRQYVAGTQHDYFHHDIIGWTRGSS 453
 OY 421 HNSGGLATMSDPCGNMWTYVGHKAGQVWRDITGNSGTVTINADGKMTYNGAVS 480
 DB 454 HNSGGLATMSDPCGNMWTYVGHKAGQVWRDITGNSGTVTINADGKMTYNGAVS 513
 OY 481 VVWQ 485
 DB 514 IWNK 518

RESULT 2
 AMT_BACLI STANDARD: PRT: 512 AA.

AC P06278;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE ALPHA-AMYLASE PRECURSOR (EC 3.2.1.1) (1,4-ALPHA-D-GLUCAN
 DE GLUCANOHYDROLASE).
 GN AMYS OR AMYL.
 OS Bacillus licheniformis.
 OS Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Bacillus.
 OC NCBI_TaxID=1402;
 RP [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=66115694; PubMed=2418011;
 RA YUUKI T., Nomura T., Tezuka H., Tsuboi A., Yamagata H.,
 RA Tsukagoshi N., Uda S.;
 RT "Complete nucleotide sequence of a gene coding for heat- and
 RT pH-stable alpha-amylase of Bacillus licheniformis: comparison of the
 RT amino acid sequences of three bacterial liquefying alpha-amylases
 RT deduced from the DNA sequences.";
 RL J. Biochem. 98:1147-1156(1985).
 RP [2]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=86135857; PubMed=3009417;
 RA Gray G.L., Mainzer S.E., Rey M.W., Lamsa M.H., Kindle K.L.,
 RA Carmona C., Requadt C.;
 RT "Structural genes encoding the thermophilic alpha-amylases of
 RT Bacillus stearothermophilus and Bacillus licheniformis.";
 RL J. Bacteriol. 166:635-643(1986).
 RP [3]
 RP SEQUENCE OF 1-104 FROM N.A.
 RC MEDLINE=84185455; PubMed=6609154;
 RA Stephens N.A., Orlepp S.A., Ollington J.F., McConnell D.J.;
 RT "Nucleotide sequence of the 5' region of the Bacillus licheniformis
 RT alpha-amylase gene: comparison with the B. amyloliquefaciens gene.";
 RL Bacteriol. 158:369-372(1984).

RP [4]
 RP SEQUENCE OF 1-29 FROM N.A.
 RC MEDLINE=89213924; PubMed=2540150;
 RA Lacle B.M., Chambliss G.H., McConnell D.J.;
 RT "Bacillus licheniformis alpha-amylase gene, amyL, is subject to
 RT promoter-independent catalytic repression in Bacillus subtilis.";
 RL J. Bacteriol. 171:2435-2442(1989).
 RP [5]
 RP SEQUENCE OF 30-47.
 RC MEDLINE=82098050; PubMed=6172418;
 RA Kuhn H., Fietzek P.P., Lampen J.O.;
 RT "N-terminal amino acid sequence of Bacillus licheniformis
 RT alpha-amylase: comparison with Bacillus amyloliquefaciens and
 RT Bacillus subtilis enzymes.";
 RL J. Bacteriol. 149:372-373(1982).
 RP [6]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RC STRAIN=ATCC 27811;
 RA MEDLINE=95182462; PubMed=7877175;
 RT Machius M., Wiegand G., Huber R.;
 RT "Crystal structure of calcium-depleted Bacillus licheniformis alpha-
 RT amylase at 2.2-A resolution.";
 RL J. Mol. Biol. 246:545-559(1995).
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSTS OF 1,4-ALPHA-GLUCOSIDIC
 CC LINKAGES IN OLIGOSACCHARIDES AND POLYSACCHARIDES.
 CC -1- BIOTECHNOLOGY: USED IN THE FOOD INDUSTRY FOR HIGH TEMPERATURE
 CC LIQUEFACTION OF STARCH-CONTAINING MASHES AND IN THE DETERGENT
 CC INDUSTRY TO REMOVE STARCH. SOLD UNDER THE NAME TERAMYL BY
 CC NOVOZYMES.
 CC -1- MISCELLANEOUS: ABLE TO WORK AT RELATIVELY HIGH (ALKALINE) PH
 CC VALUES (UP TO PH 11) AND AT HIGH TEMPERATURES (UP TO 100 DEGREE
 CC CELSIUS).
 CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
 CC KNOWN AS THE ALPHA-AMYLASE FAMILY.
 CC -----
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 CC or send an email to license@isb-slb.ch).
 CC -----
 DR EMBL: X03236; CAA26981.1; -
 DR EMBL: M38570; AAA22226.1; -
 DR EMBL: M13256; AAA22240.1; -
 DR EMBL: K01984; AAA22193.1; -
 DR EMBL: M26412; AAA22237.1; -
 DR EMBL: A17930; CAA01355.1; -
 DR PIR: A00844; ALBSL.
 DR PIR: B24549; B24549.
 DR PIR: A26151; A26151.
 DR PDB: 1BPL; 17-AUG-97.
 DR PDB: 1VJS; 12-MAR-97.
 DR InterPro: IPR000461; Alpha-amylase.
 DR Pfam: PF00128; alpha-amylase; 1.
 KW Hydroxylase; Glycosidase; Carbohydrate metabolism; Signal; 3D-structure.
 FT SIGNAL 1 29
 FT CHAIN 30 512
 FT ACT_SITE 260 260
 FT ACT_SITE 264 264
 FT ACT_SITE 357 357
 FT CONFLICT 38 38
 FT CONFLICT 163 163
 FT CONFLICT 339 339
 FT CONFLICT 349 349
 FT SEQUENCE 512 AA; 58549 MW; D8BB7759CD4C482 CRC64;
 Query Match 70.3%; Score 1906; DB 1; Length 512;
 Best local Similarity 69.1%; Pred. No. 9,6e-123;
 Matches 335; Conservative 67; Mismatches 73; Indels 10; Gaps 4;

63	DLGEFDQKSGIPTKYGDKAOLLAIDAALAKRNDIAVLDDVVVNHKMGADKEATRVQRVNA	122
125	SNRNOEISGETYATEAWTKFDPGRGNTSHSNFKWRWYHFDGTDWDQSRQJONKIYKFRG--	182
123	DRQTQIDEEIECEGWTRYTFPARAGYSQFIWDFKCFSGIDHIENPD-BDGIFKIVNDY	181
183	TGRKAWDEVDIENGNDYLMYADIDMDHPVINELRNMGVYVNTLNLGDFRIDAVKHK	242
182	TGEGWNPQVDELGNFDYLMGENIDFRNHAVTEIKYWARVWEQTCQDGRDLDAVKHIP	241
243	YSYTRDMLTHVRNRTGKPMFAVAFWKNDLAAIENYLNKTSWNHSVDFVPLHLYNASN	302
242	ANFYKWEIHEVQVAPKPLFIVAIEYWSHEVDKLTQYIDQVEGKTMLPDAPLQMKFHEASR	301
303	SGGYFDMRNILNGSVQKHPIHATVFDNHDSDQGEALESFVQSWFKPLAYALITLREOG	362
302	MGRDYDMTQFTGTLEADPFHATVTLVANHDTPQLQLEAPVEPWFKPLAYALILLRENG	361
363	YPSVFYGDYGIPTGHVPS-----MKSIDPLQLQARTYAYQTQHDYDFDHHDIIG	412
362	VPSVFYDLYGAHYEDVGGDQTPYIDMPITEQLDELILARQFAHGVTLPFFDHPNCIA	421
413	WTRGDSHPNSGLATIMSDGPGGNKMYVKKHAGQVWRDITGNRSGTVTINADGNGNF	472
422	FSRSGTDEFP--GCVVVMSNGDGEKTHLGENYGNKTRDFLGNRQVRYTVDENGATF	479
473	TVNGGAVSVWV 483	
480	FCNGGVSVMV 490	
<p>RESULT 7</p> <p>AMTB_PAPEO STANDARD; PRT: 1196 AA.</p> <p>ID AMTB_PAPEO</p> <p>AC P21543;</p> <p>DT 01-MAY-1991 (Rel. 18, Created)</p> <p>DT 01-MAY-1991 (Rel. 18, Last sequence update)</p> <p>DT 15-JUL-1999 (Rel. 38, Last annotation update)</p> <p>DE BETA/ALPHA-AMYLASE PRECURSOR (INCLUDES: BETA-AMYLASE (EC 3.2.1.2); ALPHA-AMYLASE (EC 3.2.1.1))</p> <p>OS Paenibacillus polymyxa (Bacillus polymyxa).</p> <p>OC Bacteria; Firmicutes; Bacillus/Clostridium group;</p> <p>OC Bacillus/Staphylococcus group; Paenibacillus.</p> <p>OX NCBI_TaxID=1406;</p> <p>RN [1]</p> <p>RN SEQUENCE OF 1-936 FROM N.A., AND PARTIAL SEQUENCE.</p> <p>RP STRAIN=72;</p> <p>RX MEDLINE=87165765; PubMed=2435707;</p> <p>RA Kawazu T., Nakanishi Y., Uozumi N., Sasaki T., Yamagata H.,</p> <p>RA Tsukagoshi N., Udaoka S.;</p> <p>RT "Cloning and nucleotide sequence of the gene coding for enzymatically active fragments of the Bacillus polymyxa beta-amylase.";</p> <p>RL J. Bacteriol. 169:1564-1570(1987).</p> <p>RN [2]</p> <p>RN SEQUENCE OF 689-1196 FROM N.A., AND PARTIAL SEQUENCE.</p> <p>RP STRAIN=72;</p> <p>RX MEDLINE=89123046; PubMed=2464578;</p> <p>RA Uozumi N., Sakurai K., Sasaki T., Takekawa S., Yamagata H.,</p> <p>RA Tsukagoshi N., Udaoka S.;</p> <p>RT "A single gene directs synthesis of a precursor protein with beta- and alpha-amylase activities in Bacillus polymyxa.";</p> <p>RL J. Bacteriol. 171:375-382(1989).</p> <p>RN [3]</p> <p>RN SEQUENCE OF 1-776 FROM N.A.</p> <p>RP STRAIN=ATCC 8523;</p> <p>RX MEDLINE=87231094; PubMed=2438660;</p> <p>RA Rhodes C., Strasser J., Friedberg F.;</p> <p>RT "Sequence of an active fragment of B. polymyxa beta amylase.";</p> <p>RL Nucleic Acids Res. 15:3934-3934(1987).</p> <p>RN [4]</p> <p>RN DISULFIDE BOND, AND MUTAGENESIS OF CYSTEINES.</p> <p>RX MEDLINE=91215008; PubMed=1827035;</p> <p>RA Uozumi N., Matsuda T., Tsukagoshi N., Udaoka S.;</p>		

Structural and functional roles of cysteine residues of Bacillus polymyxa beta-amylase.;
 Biochemistry 30:4594-4599(1991).
 CC -1- FUNCTION: THE PRECURSOR PROTEIN IS PROTEOLITICALLY CLEAVED TO PRODUCE MULTIFORM BETA-AMYLASES AND A 48 KDA ALPHA-AMYLASE AFTER SECRETION.
 CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF 1,4-ALPHA-GLUCOSIDIC LINKAGES IN POLYSACCHARIDES SO AS TO REMOVE SUCCESSIVE MALTOSE UNITS FROM THE NON-REDUCING ENDS OF THE CHAINS.
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-ALPHA-GLUCOSIDIC LINKAGES IN OLIGOSACCHARIDES AND POLYSACCHARIDES.
 CC -1- SUBCELLULAR LOCATION: SECRETED.
 CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO FAMILY 14 OF GLYCOSYL HYDROLASES (BETA-AMYLASES).
 CC -1- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.
 CC -----
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 CC -----
 DR EMBL; M15817; AAA85446.1; -;
 DR EMBL; Y00150; CAA68344.1; -;
 DR PIR; A29130; A29130.
 DR PIR; A29108; A29108.
 DR PIR; A32251; A32251.
 DR HSP; P43379; ITCM.
 DR InterPro; IPR000461; Alpha_amylase.
 DR InterPro; IPR001554; Glyco_hydro_14.
 DR Pfam; PF00128; alpha-amylase; 1.
 DR Pfam; PF01373; Glyco_hydro_14; 1.
 DR PRINTS; PR00750; BETAAMYLASE.
 DR PRINTS; PR00841; GLHYDLASE14.
 DR PROSITE; PS00506; BETA_AMYLASE_1; 1.
 DR PROSITE; PS00679; BETA_AMYLASE_2; 1.
 KW Multifunctional enzyme; Hydrolase; Glycosidase; Signal;
 KW Polysaccharide degradation; Repeat.
 FT SIGNAL 1 35
 FT CHAIN 36 1196 BETA/ALPHA-AMYLASE.
 FT DOMAIN 36 454 BETA-AMYLASE.
 FT REPEAT 455 558
 FT REPEAT 559 668
 FT DOMAIN 669 1196
 FT DSULFID 118 126
 FT ACT_SITE 124 124
 FT ACT_SITE 198 198
 FT MUTAGEN 118 118
 FT MUTAGEN 126 126
 FT MUTAGEN 358 358
 FT CONFLICT 1 1
 FT CONFLICT 67 67
 FT CONFLICT 100 100
 FT CONFLICT 154 154
 FT CONFLICT 177 177
 FT CONFLICT 227 228
 FT CONFLICT 330 330
 FT CONFLICT 425 425
 FT CONFLICT 493 493
 FT CONFLICT 532 532
 FT CONFLICT 559 559
 FT CONFLICT 665 665
 FT CONFLICT 681 681
 FT CONFLICT 686 686
 FT CONFLICT 725 728
 FT CONFLICT 736 736
 FT CONFLICT 741 741
 FT CONFLICT 758 758
 FT SEQUENCE 1196 AA; 130893 MW; A41EA6B70E257064 CRC64;

Query Match 11.6%; Score 315; DB 1; Length 1196;
 Best Local Similarity 24.1%; Pred. No. 5.5e-14;
 Matches 125; Conservative 67; Mismatches 189; Indels 138; Gaps 25;
 QY 1 HHNTGNTMOMYFEWHLPNDGNHNRRLDDAANLKSGITAVWIPPAWKGTQNDV-GYG 59
 DB 766 NYGFGNNSDQRKWH-----GGDFQGLQINKLDYIKNGMGTAIWITPTVMQKSEYAHGYH 821
 QY 60 AYDLYDLGEFNOKGTVTYKTKYRSQLOGAVTSLKNNGIOYGVVVMNHKKGADGETMVNA 119
 DB 822 TYDFY-----AVDGHGLGTMDKLQELVRKAHDKIAVMVDDVVAHTG----- 862
 QY 120 VEVNRSNRNQEISGEYTIETAWTKDF-PGRGNTHSNF-KWRVYHFDG--TDWDQSRQLQN 175
 DB 863 -----DFQPGNGFAKAPDKADWYHHNGDITDGDYNSNQ- 897
 QY 176 KIYFRGTGKAWDEVDIENGNYDLYMADIOMDHPVINELRNMGVYNTNLTLDGFRI 235
 DB 898 -----WK--IENG--DVAGLDLNLHENPATANELKNWIKWLLNETGIDGLRL 940
 QY 236 DAVKHIKYSYTRDWLTHVRNTTGKPMFAVAFAEFKNDLAAIENYLNKTSWNHSHVDFDPLHY 295
 DB 941 DTAKHVPKGLKDF-DQAANT-----FTMGEIFHGDPAIYVGDY---TRYLDAALDFPMY 991
 QY 296 NLYNASNSGGYDFMNRILNGSVQKHPIHVT---FVDNHD-----SOPGEALESF 343
 DB 992 TIKDV--FGHDSMRKIKDRYSDDRYRDAGTNGVFDNHDVKKFLNDASGKPGANYDKW 1049
 QY 344 VQSWFKPLAYALILT-REQGYPSVFGYGYGIPHTGVPSMKSIDPLLQARQTYAGTQH 402
 DB 1050 PQ-----LKAALGFTLTSRGIPITTYQGTQYSGGDDPA-----NRENNMFNANH 1094
 QY 403 DYFDHDIIGTWREGSSHPNSGLATIMSDGPGCKNKM-----YVGKHKAG-----Q 449
 DB 1095 DLYOIAKLNIVR---NNHP-----ALQNSQREKVVDDSFYSFQSKNGDEAIVFINN 1145
 QY 450 VWRDIT---GN-----RSGTVTINADGNGFTVNGGAVSV 481
 DB 1146 SWNSQTRTIGNFDNLNCTRLTNLSNDSVQINGNSITV 1184
 RESULT 8
 AM3A_ORYSA
 ID AM3A_ORYSA STANDARD; PRT; 440 AA.
 AC P27932;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE ALPHA-AMYLASE ISOZYME 3A PRECURSOR (EC 3.2.1.1) (1,4-ALPHA-D-GLUCAN GLUCANOHYDROLASE).
 GN AMY1.2 OR AMY3A.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
 CX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. JAPONICA M202; TISSUE=Etiolated leaf;
 RX MEDLINE=91329692; PubMed=1714318;
 RA Sutliff T.D., Huang N., Litts J.C., Rodriguez R.L.;
 RT "Characterization of an alpha-amylase multigene cluster in rice.";
 RL Plant Mol. Biol. 16:579-591(1991).
 CC -1- FUNCTION: IMPORTANT FOR BREAKDOWN OF ENDOSPERM STARCH DURING GERMINATION.
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-ALPHA-GLUCOSIDIC LINKAGES IN OLIGOSACCHARIDES AND POLYSACCHARIDES.
 CC -1- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
 CC -1- SUBUNIT: MONOMER.
 CC -1- TISSUE SPECIFICITY: MOST ABUNDANT IN EMBRYO-DERIVED CALLUS TISSUE.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED AT A HIGH LEVEL DURING GERMINATION IN THE ALEURONES CELLS UNDER THE CONTROL OF THE PLANT HORMONE

CC	GIBBERELIC ACID AND IN THE DEVELOPING GRAINS AT A LOW LEVEL.
CC	-!- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
CC	KNOWN AS THE ALPHA-AMYLASE FAMILY.
CC	-----
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CC	or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL; X56336; CAA39776.1; -
DR	PIR; S14958; S14958.
DR	HSP; P04063; IAMY.
DR	Mendel; 9689; Orysa; Amy1.2.
DR	InterPro; IPR000461; Alpha-amylase.
DR	Hydrolase; Glycosidase; Carbohydrate metabolism; Calcium; Signal;
KW	Multigene family.
FT	SIGNAL 1 26
FT	CHAIN 27 440
FT	ACT_SITE 207 207
FT	ACT_SITE 315 315
FT	CA_BIND 119 119
FT	CA_BIND 178 178
FT	SEQUENCE 440 AA; 48872 MW; 5E9B78C29AA91C2B CRC64;
SQ	-----
CC	Query Match 10.8%; Score 294; DB 1; Length 440;
CC	Best Local Similarity 25.8%; Pred. No. 4.5e-13;
CC	Matches 106; Conservative 56; Mismatches 151; Indels 98; Gaps 18;
QY	9 MMYQFEW-HLPDNGHNWRLRDDAANKLSKGIITAVWTPPAWKTSQNDVGYGAYDLYDLG 67
DB	31 LFQGFNDSWKKGQGWYMLKDQVGDIAAGVTHWLPPTTHSVSQ--GYMPCRLYDLN 88
QY	68 EFNKGIVRTKYGRSOLQAVTSLKNGIQVYGDVVMNHKGGADGTEMYNAVEVNSRN 127
DB	89 -----ASKYGTAKELSLIAAFHAKGKICVADIVNHCADD----- 125
QY	128 NOETISGEYTTIEMTKFPFGRGNTHSNFKRWYHFDGTDQDQSLQNLKIKYPRGTGKAW 187
DB	126 -KDRGVIYCI-----FKGGPRG-----LDWGPMSICDDTQYSDGTGH-- 164
QY	188 DWEVDIENGNDYLMYADIDMDHPEVINELRNMGVYVNTLNLDFRIDAVKHKYSYTR 247
DB	165 -----RDTGADFAAPDIDHNLPLVQRELSDLRLRLRDVGDGWLDFAKGYSAAVAR 218
QY	248 DMLTHVNTTKPMFAVAFWKNDLA-----AIENLYNKTWNHVSFV 291
DB	219 ---TVVQN--ARPSFVVAEIW-NSLSYDGDGKPAANODGQRELNVNWKVQVGGPATAFDF 272
QY	292 PLHYNLYNASNGYGFDMRNLNG--SVQKQHPHIAVTVDNHDSDQGEALSFVQSWF 348
DB	273 TTK-GILQSAVQGELEWRNRD-KDKAPGMIGWYEPKAVTFVDNHT-----GSTQRMWP 324
QY	349 KP-----LAYALILTREOGYPSVFGYDYGIPTHGVPSMSKSIDPLQARQ 394
DB	325 FPSDKVILGYAVILT-HPGVPCIEYDQVFDW-----NLKOEINALAATRK 368
RESULT	9
ID	AMYA_VIGMU STANDARD; PRT; 421 AA.
AC	AMYA_VIGMU
DT	17859;
DT	01-AUG-1990 (Rel. 15, Created)
DT	01-AUG-1990 (Rel. 15, Last sequence update)
DT	15-DEC-1998 (Rel. 37, Last annotation update)
DE	AMYA-VIGMU PRECURSOR (EC 3.2.1.1) (1,4-ALPHA-D-GLUCAN
DE	GLUCANOHYDROLASE).
GN	AMY1.1.
Q5	Vigna mungo (Rice bean) (Black gram).

OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC	eurosid 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.
OX	NCBI_TaxID=3915;
RP	[1]
RP	SEQUENCE FROM N.A.
RP	TISSUE=Cotyledon;
RC	MEDLINE=90332425; PubMed=2377468;
RA	Yamauchi D., Minamikawa T.
FT	"Nucleotide sequence of cDNA for alpha-amylase from cotyledons of
FT	germinating Vigna mungo seeds.";
FT	Nucleic Acids Res. 18:4250-4250(1990).
FN	[2]
FN	SEQUENCE FROM N.A.
FN	MEDLINE=94120017; PubMed=8290640;
RA	Takeuchi H., Yamauchi D., Wada S., Minamikawa T.;
FT	"Nucleotide sequence of the alpha-amylase gene from Vigna mungo.";
RL	Plant Physiol. 103:1459-1459(1993)
CC	-!- CATALYTIC ACTIVITY: ENDOLYOLYSIS OF 1,4-ALPHA-GLUCOSIDIC
CC	LINKAGES IN OLIGOSACCHARIDES AND POLYSACCHARIDES.
CC	-!- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
CC	-!- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
CC	KNOWN AS THE ALPHA-AMYLASE FAMILY.
CC	-----
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC	or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL; X53049; CAA37217.1; -
DR	EMBL; X73301; CAA51734.1; -
DR	PIR; S10514; S10514.
DR	PIR; S40201; S40201.
DR	HSP; P04063; IAMY.
DR	Mendel; 12451; VIGMU; Amy1.1.
DR	InterPro; IPR000461; Alpha-amylase.
DR	Hydrolase; Glycosidase; Carbohydrate metabolism; Calcium; Signal.
KW	PROBABLE.
FT	SIGNAL 1 23
FT	CHAIN 24 421
FT	ACT_SITE 201 201
FT	ACT_SITE 309 309
FT	CA_BIND 113 113
FT	CA_BIND 172 172
FT	SEQUENCE 421 AA; 46888 MW; 15CA0DABA3DB4656 CRC64;
SQ	-----
CC	Query Match 10.6%; Score 287.5; DB 1; Length 421;
CC	Best Local Similarity 24.7%; Pred. No. 1.2e-12;
CC	Matches 99; Conservative 48; Mismatches 137; Indels 117; Gaps 14;
QY	9 MMYQFEW-HLPDNGHNWRLRDDAANKLSKGIITAVWTPPAWKTSQNDVGYGAYDLYDLG 68
DB	26 LFQGFNDSWKKGQGWYMLKDQVGDIAAGVTHWLPPTTHSVSQSVPSE--GYLPGRLYDLN 82
QY	69 FNQKIVRTKYGRSOLQAVTSLKNGIQVYGDVVMNHKGGADGTEMYNAVEVNSRN 128
DB	83 -----ASKYGNELKSLIAAFHAKGKICLADIVNH-----RTAER 119
QY	129 QEISGEYTTIEMTKFPFGRGNTHSNFKRWYHFDGTDQDQSLQNLKIKYPRGTGKAWD 188
DB	120 KDRGVIYCI-----FEG-GTPDSR-----QDWGPFICRDTTAYSDGTGN--- 158
QY	189 WEVDIENGNDYLMYADIDMDHPEVINELRNMGVYVNTLNLDFRIDAVKHKYSYTRD 248
DB	159 -----NDSGGGYDAAPDIDHNLPLVQRELSSEWNWLKTEICFDGWRDFVKGYAPSIKI 213
QY	249 WLTHVNTTKPMFAVAFW-----KNDLAAIENLYNKTWNHVSFVDP 293
DB	214 YMEQT-----KPDFAVGEKWDTSYSGDGKPNYNQDQSHRGALVNWVESAGAITAFD--- 265


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Db 326 QHFWALQDGLIROAYAYILT-SPGTPVYVWVSHMYDMWYGDF-----IRQLI 370
QY 391 QARQYVYGTQHDYFDHDIIGTWREGDSHPNSGLATIMSDGPGGNKMYV----- 442
Db 371 QVRR--AAGVRAD-----SASFH--SGYSLVATVSGSQTLVVALNSDLGN 414
QY 443 -GKHKAG-----QVRDITGNRSG 460
Db 415 PGQVAGSFSEAVNASGQVRWRSRGSGGG 446

RESULT 11
AMT4_PSEA
ID AMT4_PSEA STANDARD; PRT; 551 AA.
AC P22963;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE GLUCAN 1,4-ALPHA-MALTOTETRAHYDROLASE PRECURSOR (EC 3.2.1.60) (G4-
DE AMYLASE) (MALTOTETRAOSE-FORMING AMYLASE) (EXO-MALTOTETRAHYDROLASE)
DE (MALTOTETRAOSE-FORMING EXO-AMYLASE).
GN MTA.
OS Pseudomonas saccharophila.
OC Bacteria; Proteobacteria; beta subdivision; Comamonadaceae.
OX NCBI_TaxID=304;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=IAM 1504;
RX MEDLINE=90005970; PubMed=2676600;
RA Zhou J., Baba T., Takano T., Kobayashi S., Arai Y.;
RT "Nucleotide sequence of the maltotetraohydrolase gene from
RT Pseudomonas saccharophila.";
RL FEBS Lett. 255:37-41(1989).
CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF 1,4-ALPHA-D-GLUCOSIDIC LINKAGES
CC IN AMYLACEOUS POLYSACCHARIDES SO AS TO REMOVE SUCCESSIVE
CC MALTOTETRAOSE RESIDUES FROM THE NON-REDUCING CHAIN ENDS.
CC -1- COFACTOR: BINDS TWO CALCIUM IONS (BY SIMILARITY).
CC -1- PATHWAY: DEGRADATION OF STARCH.
CC -1- SUBCELLULAR LOCATION: SECRETED.
CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
CC KNOWN AS THE ALPHA-AMYLASE FAMILY.
-----
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or send an email to license@isb-sib.ch).
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DR EMBL: X16732; CAA34708.1; -
DR PIR: S05667; S05667.
DR HSP: F13507; 2AMG.
DR InterPro: IPR000461; Alpha_amylase.
DR Pfam: IPR002044; CBD_4.
DR Pfam: PF00128; alpha-amylase; 1.
DR Pfam: PF00686; CBD_4; 1.
DR ProbDom: PD001568; CBD_4; 1.
KW Hydrolase; Glycosidase; Signal; Carbohydrate metabolism; Calcium.
FT SIGNAL 1
FT CHAIN 21
FT CHAIN 22 551
FT DISULFID 161 171
FT DISULFID 237 272
FT CA_BIND 22 22
FT CA_BIND 23 23
FT CA_BIND 34 34
FT CA_BIND 37 37
FT CA_BIND 38 38
FT CA_BIND 137 137
FT CA_BIND 172 172
FT CA_BIND 175 175
FT CA_BIND 183 183
FT CA_BIND 214 214
FT ACT_SITE 214
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FT ACT_SITE 240 240 BY SIMILARITY.
FT ACT_SITE 315 315 BY SIMILARITY.
SQ SEQUENCE 551 AA; 59898 MW; F6D67DOBB235EA35 CRC64;

Query Match 10.4%; Score 283.5; DB 1; Length 551;
Best Local Similarity 24.8%; Pred. No. 3.le-12;
Matches 131; Conservative 62; Mismatches 183; Indels 153; Gaps 23;

QY 2 HNGTNGTMQYFEWHL-----PNDGNHNRLRDAANLKSIGITAVWIPPAWK----- 49
Db 33 YHGDEIILQGFHNVVREAPND--WYNILRQQAASIAADGFSAIWMPVWRPWFSSWTGD 90
QY 50 GTSQNDVYGAYDLYDIGEFNQKGTVRTKGTYSQLOGAVTSKNGNGIQYGVGVVNHKG 109
Db 91 GKSGGEGYFWHD-----FNKNG---RYGSDAQLRQAAGALGGAGVKVLYDVPNH-- 138
QY 110 GADTEWNAVEVNRNNOEISGEYIEAWTKFDFPGRGNTHSNFKRWYHFDGTDWDQ 169
Db 139 -----MNRGYPDKREINLPACQGFW-RNDCADPGN-----YPNDCDDGD- 175
QY 170 SRQLQNKIYKFRGTGKAWDWEVDIENGNYDLYMAYADIMDHPEVINELRNNGVWYNTLN 229
Db 176 -----RFIG-GE-----SDLNTGHPQI-----YGMFRDELAN 201
QY 230 L-----DGFRIADVKKIKSYTRDWLTHVNTTKPKMFAVAEFKNDLAAIE-NYLNKT 282
Db 202 LRSGYGAGGFRDFVRGYAPERVDSDMSDSADSS-----FCVGLWKGFSEYPSWDWNTA 257
QY 283 SWNH-----SVFDVPLHYNLNASNGGYFDMRNILNGSVVQKHPIHATVFDN 331
Db 258 SWQIILKWSDRKPCPFDFALKERMQN---GSVADWKHGLNGNPDPRWRREVAFTVDN 313
QY 332 HDS-----QPGEALESFVQSWFKPLAYLILITREGQYSVF-----YGDYXGIPTHG 378
Db 314 HDTGYSPGNGQGHQHWALQDGLIRQAYAYILT-SPGTPVYVWVSHMYDMWYGDF----- 365
QY 379 VFSMSKSIDPLQARQTVAYGTQHDYFDHDIIGTWREGDSHP-----NSGLATIMSD 432
Db 366 -----IRQLIQRVTRAGVRADSAISFHSYSGLVATVATVSGSQTLVVALNSDLANPGQV 418
QY 433 GPGGNKMYVYVGHKAGQVWRDITGNRSRGTVTINADGNGNFTVNGGAVSV 481
Db 419 ASGSFSEAVNASGQVRWRSRG-----DGGNGDGGEGGLNVV 457

RESULT 12
AMT4_PSEA
ID AMT4_PSEA STANDARD; PRT; 713 AA.
AC P17692;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE RAW-STARCH-DIGESTING AMYLASE PRECURSOR (EC 3.2.1.1) (1,4-ALPHA-D-
DE GLUCAN GLUCANOHYDROLASE).
OS Bacillus sp. (strain B1018).
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1417;
RN [1]
SEQUENCE FROM N.A., AND SEQUENCE OF 28-47.
RX MEDLINE=90147765; PubMed=1689153;
RA Itokor P., Tsukagoshi N., Uda S.;
RT "Nucleotide sequence of the raw-starch-digesting amylase gene from
RT Bacillus sp. B1018 and its strong homology to the cyclodextrin
RT glucanotransferase genes.";
RL Biochem. Biophys. Res. Commun. 166:630-636(1990).
CC -1- FUNCTION: THIS ENDO-TYPE ADSORBABLE AMYLASE IS CAPABLE TO
CC DIGEST RAW-STARCH.
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-ALPHA-GLUCOSIDIC
CC LINKAGES IN OLIGOSACCHARIDES AND POLYSACCHARIDES.
CC -1- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
CC -1- SUBCELLULAR LOCATION: SECRETED.
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CC	SEQUENCE	713 AA; 78340 MW; 524B259526B56C52 CRC64;	
CC	Query Match	10.1%; Score 275; DB 1; Length 712;	
CC	Best Local Similarity	22.4%; Pred. No. 1.6e-11;	
CC	Matches 114; Conservative	90; Mismatches 190; Indels 114; Gaps 27;	
QY	21	GNHW-----NLRDRAANLKSGLTAVWIPP-----AMKGTSONDVGYGAYDLYDLGFEFNQK 72	
DB	78	GDWQGGIINKIND--GYLTGMGTITAIWISQPVENIYVINGVHTAYHGYWADFKK- 134	
QY	73	GTVRTKYGTRSQLQCAVTSKNGINGIQVYGVDMVNMHKGADGTEMVNAVVENNRNOEIS 132	
DB	135	--TNPAYGTMQDFKNLIDTAHAIKVIIDFAPNHTSPASSDD--PSFAENGRLYDNGNLL 191	
QY	133	GEYITIAWTKFDPGRCNTHSNFKRWYHFDGTDWDSROLQNKIKYKFRGTGKAWDEVD 192	
DB	192	GGYTNDTQNLF-----HHYGGTDFS---TIENGIYK-----NLYDL-AD 226	
QY	193	TEENGYDLYMAYDMDHPEVINELRNMGVWYNTNLNLDGFRIDAVKHIKYSTRMLTH 252	
DB	227	LNHN-----SSVDVYLKDAIK-----MWL--DLGVDGIRVDVAKHMPFGWQKSPMST 272	
QY	253	VRNTGKPMFAVAFW--KNDLA-AIENYLNKISWNHSVDFVPLHYNLYNA--SNSGGYF 307	
DB	273	INNY--KPVFNFGWFLGVNEISPEYHOFANESGM--SLLDFFPAQAKARQVFRONTNMY 328	
QY	308	DMRNILNGSVVQKPIH-AVTFVDNHDSSQPGEALESFVQSFVKPLAYALILTREQGYPSV 366	
CC	OF A 1,4-ALPHA-D-GLUCOSIDIC BOND.		
CC	-1- COFACTOR: BINDS TWO CALCIUM IONS.		
CC	-1- SUBUNIT: MONOMER.		
CC	-1- MISCELLANEOUS: CGTASE MAY CLEAVE TWO PROTEIN DOMAINS: THE ONE		
CC	IN THE AMINO-TERMINAL SIDE CLEAVES THE ALPHA-1,4-GLUCOSIDIC BOND		
CC	IN STARCH, AND THE OTHER IN THE C-TERMINAL SIDE CATALYZES OTHER		
CC	ACTIVITIES, INCLUDING THE RECONSTITUTION OF AN		
CC	ALPHA-1,4-GLUCOSIDIC LINKAGE FOR CYCLIZING THE		
CC	MALTOOLIGOSACCHARIDE PRODUCED.		
CC	-1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO		
CC	KNOWN AS THE ALPHA-AMYLASE FAMILY.		
CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration		
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -		
CC	the European Bioinformatics Institute. There are no restrictions on its		
CC	use by non-profit institutions as long as its content is in no way		
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CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/		
CC	or send an email to license@isb-sib.ch).		
CC	EMBL; M19880; AAA22309.1; -		
DR	EMBL; D00129; BAA00077.1; -		
DR	PIR; S24193; ALBSG3.		
DR	HSP; P05618; LPAM.		
DR	InterPro; IPR000461; Alpha_amylase.		
DR	InterPro; IPR002044; CBD_4.		
DR	InterPro; IPR002909; IPT_TIG.		
DR	Pfam; PF00128; alpha-amylase; 1.		
DR	Pfam; PF00686; CBD_4; 1.		
DR	Pfam; PF01833; TIG; 1.		
DR	ProDom; PD001568; CBD_4; 1.		
DR	Transferrase; Glycosyltransferase; Calcium; Signal.		
KW	SIGNAL		
FT	CHAIN	28 712	CYCLOMALTODEXTRIN GLUCANOTRANSFERASE.
FT	DOMAIN	28 165	A1.
FT	DOMAIN	166 229	B.
FT	DOMAIN	230 433	A2.
FT	DOMAIN	434 522	C.
FT	DOMAIN	523 608	D.
FT	DOMAIN	609 712	E.
FT	DISULFID	70 77	BY SIMILARITY.
FT	ACT_SITE	256 256	BY SIMILARITY.
FT	ACT_SITE	284 284	BY SIMILARITY.
FT	ACT_SITE	355 355	BY SIMILARITY.
FT	CONFLICT	582 586	VPGGI -> SWRHL (IN REF. 2).
QY	SEQUENCE	712 AA; 78249 MW; 4FAA8F70BEF818F9 CRC64;	
CC	Query Match	10.1%; Score 275; DB 1; Length 712;	
CC	Best Local Similarity	22.4%; Pred. No. 1.6e-11;	
CC	Matches 114; Conservative	90; Mismatches 190; Indels 114; Gaps 27;	
QY	21	GNHW-----NLRDRAANLKSGLTAVWIPP-----AMKGTSONDVGYGAYDLYDLGFEFNQK 72	
DB	78	GDWQGGIINKIND--GYLTGMGTITAIWISQPVENIYVINGVHTAYHGYWADFKK- 134	
QY	73	GTVRTKYGTRSQLQCAVTSKNGINGIQVYGVDMVNMHKGADGTEMVNAVVENNRNOEIS 132	
DB	135	--TNPAYGTMQDFKNLIDTAHAIKVIIDFAPNHTSPASSDD--PSFAENGRLYDNGNLL 191	
QY	133	GEYITIAWTKFDPGRCNTHSNFKRWYHFDGTDWDSROLQNKIKYKFRGTGKAWDEVD 192	
DB	192	GGYTNDTQNLF-----HHYGGTDFS---TIENGIYK-----NLYDL-AD 226	
QY	193	TEENGYDLYMAYDMDHPEVINELRNMGVWYNTNLNLDGFRIDAVKHIKYSTRMLTH 252	
DB	227	LNHN-----SSVDVYLKDAIK-----MWL--DLGVDGIRVDVAKHMPFGWQKSPMST 272	
QY	253	VRNTGKPMFAVAFW--KNDLA-AIENYLNKISWNHSVDFVPLHYNLYNA--SNSGGYF 307	
DB	273	INNY--KPVFNFGWFLGVNEISPEYHOFANESGM--SLLDFFPAQAKARQVFRONTNMY 328	
QY	308	DMRNILNGSVVQKPIH-AVTFVDNHDSSQPGEALESFVQSFVKPLAYALILTREQGYPSV 366	

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Db 329 GLKAMLEGSEVDYAQVNDQVTFIDNHDMEFHTSNGDRKLEQALFTL--TSRGVPAI 385
Oy 367 EVG-DYY-----GITHGVPS-----MKSIDPLLOARQTYAGTQHDYFDHDI 410
Db 386 YGSEQYSGGNDPDNRARISFSTTTAYQVIOKLAPRKSNAIPAAYGSGTOERWINDV 445
Oy 411 IGWTFE-----GDSSHPNS--GLATIMSDPGGKMKWYVGHKKAQGVNRDITGN 457
Db 446 IYERKFNNAVVAIVNMMTPASITGLVTSLPQGS-----YNDVLGG 489
Oy 458 --RSTVTVINADG-WGNTVNGVAGVSW 482
Db 490 ILNGNTLTAVGGAASNETLAPGGTAVW 517

RESULT 15
CDGT_BACCI STANDARD; PRT; 718 AA.
AC P30920;
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE CYCLOMALTODEXTRIN GLUCANOTRANSFERASE PRECURSOR (EC 2.4.1.19)
DE (CYCLODEXTRIN-GLYCOSYLTRANSFERASE) (CGTASE).
OS Bacillus circulans.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID-1397;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=8;
RA Nitschke L., Heeger K., Bender H., Schulz G.E.;
RT "Molecular cloning, nucleotide sequence and expression in Escherichia coli of the beta-cyclodextrin glycosyltransferase gene from Bacillus circulans strain no. 8.";
RT Appl. Microbiol. Biotechnol. 33:542-546(1990).
RL [2]
RN J. Mol. Biol. 217:737-750(1991).
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RC STRAIN=8;
RX MEDLINE-911171298; PubMed-1826034;
RA Klein C., Schulz G.E.;
RT "Structure of cyclodextrin glycosyltransferase refined at 2.0-A resolution.";
RL J. Mol. Biol. 209:793-800(1989).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (3.4 ANGSTROMS).
RC STRAIN=8;
RX MEDLINE-90064533; PubMed-2531228;
RA Hofmann B.E., Bender H., Schulz G.E.;
RT "Three-dimensional structure of cyclodextrin glycosyltransferase from Bacillus circulans at 3.4-A resolution.";
RL J. Mol. Biol. 209:793-800(1989).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
RC STRAIN=8;
RX MEDLINE-98226626; PubMed-9558324;
RA Schmidt A.K., Cottaz S., Driquez H., Schulz G.E.;
RT "Structure of cyclodextrin glycosyltransferase complexed with a derivative of its main product beta-cyclodextrin.";
RL Biochemistry 37:5909-5915(1998).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
RC STRAIN=8;
RX MEDLINE-98409292; PubMed-9738912;
RA Parsiegla G., Schmidt A.K., Schulz G.E.;
RT "Substrate binding to a cyclodextrin glycosyltransferase and mutations increasing the gamma-cyclodextrin production.";
RL Eur. J. Biochem. 255:710-717(1998).
CC -1- CATALYTIC ACTIVITY: DEGRADE STARCH TO CYCLODEXTRINS BY FORMATION
CC OF A 1,4-ALPHA-D-GLUCOSIDIC BOND.
CC -1- COPACTOR: BINDS TWO CALCIUM IONS.

-1- SUBUNIT: MONOMER.
-1- MISCELLANEOUS: CGTASE MAY CONSIST OF TWO PROTEIN DOMAINS: THE ONE IN THE AMINO-TERMINAL SIDE CLEAVES THE ALPHA-1,4-GLUCOSIDIC BOND IN STARCH, AND THE OTHER IN THE C-TERMINAL SIDE CATALYZES OTHER ACTIVITIES, INCLUDING THE RECONSTITUTION OF AN ALPHA-1,4-GLUCOSIDIC LINKAGE FOR CYCLIZING THE MALTOOLIGOSACCHARIDE PRODUCED.
-1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.
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EMBL; X68326; CAA48401.1; -.
PIR; S23674; ALBSGC.
PDB; 1CGT; 31-JAN-94.
PDB; 1CGU; 31-JAN-94.
PDB; 3CGT; 27-MAY-98.
PDB; 4CGT; 12-AUG-98.
PDB; 5CGT; 12-AUG-98.
PDB; 6CGT; 12-AUG-98.
PDB; 7CGT; 12-AUG-98.
PDB; 8CGT; 14-OCT-98.
PDB; 9CGT; 14-OCT-98.
InterPro; IPR000461; Alpha_amylase.
InterPro; IPR002044; CBD_4.
InterPro; IPR002909; IPT_TIG.
Pfam; PF001128; alpha-amylase; 1.
Pfam; PF00686; CBD_4; 1.
Pfam; PF01833; TIG; 1.
ProDom; PD001568; CBD_4; 1.
Transferase; Glycosyltransferase; Calcium; Signal; 3D-structure.
FT SIGNAL 1 34
FT CHAIN 35 718 CYCLOMALTODEXTRIN GLUCANOTRANSFERASE.
FT DOMAIN 35 172 A1.
FT DOMAIN 173 236 B.
FT DOMAIN 237 440 A2.
FT DOMAIN 441 528 C.
FT DOMAIN 529 614 D.
FT DOMAIN 615 718 E.
FT DISULFID 77 84
FT ACT_SITE 258
FT ACT_SITE 291
FT ACT_SITE 362
FT TURN 40 41
FT TURN 43 44
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FT STRAND 51 53
FT HELIX 56 59
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FT TURN 104 104
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FT STRAND 121 123
FT STRAND 124 125
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FT TURN 131 132
FT STRAND 136 142
FT TURN 144 146
FT HELIX 149 161
FT TURN 162
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Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	2410.5	88.8	518	1	A27705	alpha-amylase (EC
2	1910.5	70.4	549	1	A54541	alpha-amylase (EC
3	1906	70.3	512	1	ALBSL	alpha-amylase (EC
4	1900.5	70.1	549	1	A24549	alpha-amylase (EC
5	1894.5	69.8	549	1	A24436	alpha-amylase (EC
6	1843	67.9	514	1	ALBSN	alpha-amylase (EC
7	1833	67.6	548	1	ALBSF	alpha-amylase (EC
8	1347	49.6	493	2	S15713	alpha-amylase (EC
9	1133	41.8	491	2	C86781	alpha-amylase (EC
10	1053	38.8	494	1	B45738	alpha-amylase (EC
11	1032	37.7	495	1	A45738	alpha-amylase (EC
12	1006	37.1	495	2	B85810	cytoplasmic alpha
13	393.5	14.5	217	2	A19506	alpha-amylase (EC
14	315	11.6	1196	2	A29130	beta-amylase (EC
15	304.5	11.2	482	2	S31478	alpha-amylase (EC
16	294	10.8	440	2	S14958	alpha-amylase (EC
17	287.5	10.6	421	2	S10514	alpha-amylase (EC
18	287	10.6	423	2	T09942	alpha-amylase (EC
19	286.5	10.6	826	2	E96720	probable alpha-am
20	283.5	10.4	551	2	S05667	glucan 1,4-alpha-m
21	281	10.4	713	2	S09196	cyclomaltodextrin
22	278	10.2	428	2	T05521	alpha-amylase (EC
23	277	10.2	713	1	ALBSG1	cyclomaltodextrin
24	275	10.1	547	2	A32803	glucan 1,4-alpha-m
25	275	10.1	712	1	ALBSG3	cyclomaltodextrin
26	274.5	10.1	718	1	ALBSG2	cyclomaltodextrin
27	271	10.0	713	2	A58800	cyclomaltodextrin
28	270	10.0	713	1	ALBSG7	cyclomaltodextrin
29	269.5	9.9	718	1	ALBSG6	cyclomaltodextrin

Thu Nov 29 10:43:50 2001

Db 274 IKYSTRDWINVRSGATGNMFAVEFKNLDGAIENLYLQKTNWHSFVDPVPLHNLXNA 333
 QY 301 SNSGGYFDMRNILNGSVGOKHPHIAVTFVDNHDSPGEALSFVQSWFKPLAYAILTR 360
 Db 334 SKSGGNYDMRNIFNGTVVQHPHSHAFTFVDNHDSPGEALSFVQSWFKPLAYAILTR 393
 QY 361 QGYPVFGDYGIPTGHGVPMSKIDPLLOARQYAYGTQHDYFDHDDIIGWTREGDSS 420
 Db 394 QGYPVFGDYGIPTGHGVPMSKIDPLLEARQYAYGTQHDYFDHDDIIGWTREGDSS 453
 QY 421 HPNSGLATIMSDGPGGNKMYGKHKAGOWRDTITGNRSGTGTINADGWNFTVNGGAVS 480
 Db 454 HPNSGLATIMSDGAGGSKMYGKHKAGOWRDTITGNRSGTGTINADGWNFTVNGGAVS 513
 QY 481 VVWK 485
 Db 514 IWNK 518

RESULT 2
 A54541
 alpha-amylase (EC 3.2.1.1) precursor - Bacillus stearothermophilus (strain DN1792)
 N:Alternate names: 1,4-alpha-D-glucan glucanohydrolase
 C:Species: Bacillus stearothermophilus
 C:Date: 28-Oct-1994 #sequence_revision 18-Aug-1995 #text_change 13-Jun-1997
 C:Accession: A54541
 R:Jorgensen, P.L.; Poulsen, G.B.; Diderichsen, B.
 FEMS Microbiol. Lett. 77, 271-276, 1991
 A:Title: Cloning of a chromosomal alpha-amylase gene from Bacillus stearothermophilus.
 A:Reference number: A54541
 A:Accession: A54541
 A:Molecule type: DNA
 A:Residues: 1-549 <OR>
 A:Cross-references: GB:X59476
 A:Experimental source: Chromosomal DNA of strain DN1792
 C:Comment: Alpha-amylase genes have been found on plasmids and in multiple copies on the
 C:Genetics:
 A:Start codon: GTG
 C:Function:
 A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A:Pathway: glycogen/starch degradation
 C:Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
 C:Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysac
 F:1-34/Domain: signal sequence #status predicted <SIG>
 F:35-549/Product: alpha-amylase #status predicted <MAT>
 F:235-368/Domain: alpha-amylase core homology <AMY>
 F:139,237,272/Binding site: calcium (Asp, Asp, His) #status predicted
 F:268,298,365/Active site: Asp, Glu, Asp #status predicted

Query Match 70.4%; Score 1910.5; DB 1; Length 549;
 Best Local Similarity 68.8%; Pred. No. 2.4e-122;
 Matches 329; Conservative 69; Mismatches 79; Indels 1; Gaps 1;

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 Db 39 NGTMMQYFEWLPDDGLTWTAVANLKSGLTAVYVPPAWKGTSONDVGAYDLYD 98
 QY 66 LGEPNOKGTVRTKYGRSLOQAGTSLKNGGIQYGVYVMNHKGADGTEMVNAVEVNR 125
 Db 99 LGEPNOKGTVRTKYGRSLOQAGTSLKNGGIQYGVYVMNHKGADGTEMVNAVEVNR 158
 QY 126 NRNQBISGEYTTAEATKFDGFRGNTWNSFKRWYHFDGTQDQSRQLONKIYFRGTGK 185
 Db 159 DRNQBISGEYTTAEATKFDGFRGNTWNSFKRWYHFDGTQDQSRQLONKIYFRGTGK 217
 QY 186 ANDWEVDIENGNDYLMYADIMDHPEVINELRNWGVVTTNLNDGFRIDAVKHIKYSY 245
 Db 218 ANDWEVDIENGNDYLMYADIMDHPEVINELRNWGVVTTNLNDGFRIDAVKHIKYSY 277
 QY 246 TRDWLTHVTRNTGKPMFAVEFKNLDGAIENLYLQKTNWHSFVDPVPLHNLXNA 305
 Db 278 FPDWLSYVRSQTKPLFTVGVWYSYDINKLHNYITKTDGTSLSFADPLHNFYATKSGG 337

QY 306 YEDMRNILNGSVGOKHPHIAVTFVDNHDSPGEALSFVQSWFKPLAYAILTR 365
 Db 338 AFDMRTMTNTLMKQDQFLAVTFVDNHDSPGEALSFVQSWFKPLAYAILTR 397
 QY 366 VFYGDYGIPTGHGVPMSKIDPLLOARQYAYGTQHDYFDHDDIIGWTREGDSS 425
 Db 398 VFYGDYGIPTGHGVPMSKIDPLLIARRDYAYGTQHDYFDHDDIIGWTREGDSS 457
 QY 426 LATIMSDGPGGNKMYGKHKAGOWRDTITGNRSGTGTINADGWNFTVNGGAVS 483
 Db 458 LAALITDGGGSKMYGKHKAGOWRDTITGNRSGTGTINADGWNFTVNGGAVS 515

RESULT 3
 ALBSL
 alpha-amylase (EC 3.2.1.1) precursor [validated] - Bacillus licheniformis
 N:Alternate names: 1,4-alpha-D-glucan glucanohydrolase
 C:Species: Bacillus licheniformis
 C:Date: 30-Jun-1987 #sequence_revision 24-Apr-1998 #text_change 15-Sep-2000
 R:Yuuiki, T.; Nomura, T.; Tezuka, H.; Tsuboi, A.; Yamagata, H.; Tsukagoshi, N.; Otake, J.
 J. Biochem. 98, 1147-1156, 1985
 A:Title: Complete nucleotide sequence of a gene coding for heat- and pH-stable alpha-
 ases deduced from the DNA sequences
 A:Reference number: A91997; MUID:86111694
 A:Accession: A91997
 A:Molecule type: DNA
 A:Residues: 1-162, 'R', 164-512 <YUU>
 A:Cross-references: GB:X03236; NID:g39551; PIDN:CAA26981.1; PID:g39552
 A:Experimental source: ATCC 27811
 R:Gray, G.L.; Mainzer, S.E.; Rey, M.W.; Lamsa, M.H.; Kindle, K.L.; Carmona, C.; Requa
 J. Bacteriol. 166, 635-643, 1986
 A:Title: Structural genes encoding the thermophilic alpha-amylases of Bacillus stearo
 A:Reference number: A91817; MUID:86195857
 A:Accession: B24549
 A:Molecule type: DNA
 A:Residues: 1-338, 'G', 340-348, 'S', 350-512 <GRA>
 A:Cross-references: GB:M13256; NID:g142510; PIDN:AAA22240.1; PID:g142511
 R:Stephens, M.A.; Ortlepp, S.A.; Ollington, J.F.; McConnell, D.J.
 J. Bacteriol. 158, 369-372, 1984
 A:Title: Nucleotide sequence of the 5' region of the Bacillus licheniformis alpha-am
 A:Reference number: A91796; MUID:84185455
 A:Accession: A91796
 A:Molecule type: DNA
 A:Residues: 1-104 <STE>
 A:Cross-references: GB:K01984; NID:g142432; PIDN:AAA22193.1; PID:g142433
 R:Sibakov, M.; Palva, I.
 Eur. J. Biochem. 145, 567-572, 1984
 A:Title: Isolation and the 5'-end nucleotide sequence of Bacillus licheniformis alpha
 A:Reference number: A21663; MUID:85076654
 A:Accession: A21663
 A:Molecule type: DNA
 A:Residues: 1-3, 'H', 5-12, 'P', 14-47, 'R', 49-61, 'V', 63, 'D', 65-67, 'VA', 70-71, 'S', 73-80, 'D
 A:Experimental source: Chromosomal DNA of ATCC 14580
 A:Note: the authors translated the codon CGT for residue 48 as Gly and GAC for residu
 R:Laide, B.M.; Chambliss, G.H.; McConnell, D.J.
 J. Bacteriol. 171, 2435-2442, 1989
 A:Title: Bacillus licheniformis alpha-amylase gene, amyL, is subject to promoter-inde
 A:Reference number: I39773; MUID:89213924
 A:Accession: I39774
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-29 <LAO>
 R:Jorgensen, P.L.; Hansen, C.K.; Poulsen, G.B.; Diderichsen, B.
 Gene 96, 37-41, 1990
 A:Title: In vivo genetic engineering: homologous recombination as a tool for plasmid
 A:Reference number: I39772; MUID:91092499
 A:Accession: I39772
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA

[illegible]

A:Accession: A91804
A:Molecule type: DNA

A: Pathway: glycogen/starch degradation
B: Description: catalyzes the hydrolysis of internal 1,4- α -D-glucosidic bonds
C: Superfamily: alpha-amylase amyloliquefaciens type; alpha-amylase core homolog

C;Keywords: glycosidase; hydrolase; polysaccharide degradation
F;200-333/Domain: alpha-amylase core homology <AMY>

```

Query Match*          49.6%; Score 1347; DB 2; Length 493;
Best Local Similarity 51.4%; Pred. No. 4e-84;
Matches 247; Conservative 73; Mismatches 153; Indels 8; Gaps 3;

QY 6 NGTMMQYFEHLFNDGNHNRRLDDAANKSKGITYAVWIPPAWKTSQNDVGYGAYDLYD 65
DB 4 NHTMOMFEHLAAGDHWKRLAEMAPELKAGIDFVWVPVTKAVSAEDTGYGYDLYD 63

QY 66 LGFENQKGVTRTKYGRSOLQAVTSILKNGIQVYGDVYVNNHKGADGTEMVNAVEVNR 125
DB 64 LGFEDQKGVTRTKYGRSOLQAVTSILKNGIQVYGDVYVNNHKGADGTEMVNAVEVNR 123

QY 126 NRNOEISGEYTIKAWTKFDPGRGNTHSNFKRWYHFDGTDQSDQSLQNLKIKYKRGTK 185
DB 124 DRTKEISEPTEIGTWKTFPPGRGQDYSFKNSEHFNFGTDDP-AREERTGVFRAGENK 182

QY 186 ANDWEVDIENGNDYLMVADIMDMHPEVINELRNMGVYVNTNLNLDGFRIDAVKHKYSY 245
DB 183 KWNENVDDEFGNYDILFANIDYHNPVREMDWGWKLLDITLQCGGFRIDAIKHINHEF 242

QY 246 TRDMLTHVRNTTGPMPFAVAFKNDLAATENYLNKTSWNHVSFDPVPLHLYNLNASNSG 305
DB 243 IKFEAAEMIRKRGQDFYIVGEFWSNLDACREFLDTVQIDFVLSLHYKLHEASLGR 302

QY 306 YFDMRNILNGSVQKHPHATVFDVNDHDSQPEALSFVQSWFKPLAYALILTRQOGYPS 365
DB 303 FDFLSKIFDDILVQTHPHTAVTFVDNHDSPHEALSWIGDFKPSAYALTLLRROGPV 362

QY 366 VFYDGYGI-----PHGVPSMKSIDPLLOARQYVYAGTQHDYDHDHDIIGTWREGDSSH 421
DB 363 VFYDGYGIGGPEVDG---KKEILDILLSARCNAKYGQEDYFDHANTIGWVRGVEEI 419

QY 422 PMSGGLATMSDGPCKWYVGHKAGOVWRDITGNRSCTVINADGNGFTVNGGAVSV 481
DB 420 ESGGCVNISNGDGEKRMFGEHRAGEVWDLTKSCDDQITIEDGWATPHVCGGVS 479

QY 482 W 482
DB 480 W 480

RESULT 9
C86781
alpha-amylase [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 31-Mar-2001
C;Accession: C86781
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jalllon, O.; Malarne, K.; Weissenbach, J.; Ehrlich
Genome Res. in press, 2001
A;Title: the complete genome sequence of the lactic acid bacterium.
A;Reference number: A86825
A;Accession: C86781
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-491 <STO>
A;Cross-references: GB:AE005176; NID:g12724224; PIDN:AAK05349.1; GSPDB:GN00146
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: amyl
C;Superfamily: alpha-amylase, amylioliquefaciens type; alpha-amylase core homology

Query Match          41.8%; Score 1133; DB 2; Length 491;
Best Local Similarity 43.0%; Pred. No. 1.4e-69;
Matches 205; Conservative 96; Mismatches 172; Indels 4; Gaps 3;

QY 8 TMQMOMFEHLFNDGNHNRRLDDAANKSKGITYAVWIPPAWKTS-QNDVGYGAYDLYD 66
DB 3 TILQAFWYLPDSQHNHNKINIPDLKGLFSGLWLPASPAAASGVEDVGYGYDLYD 62

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QY 67 GFENQKGVTRTKYGRSOLQAVTSILKNGIQVYGDVYVNNHKGADGTEMVNAVEVNR 126
DB 63 GFEDQKGVTRTKYGRSOLQAVTSILKNGIQVYGDVYVNNHKGADGTEMVNAVEVNR 122

QY 127 RNOEISGEYTIKAWTKFDPGRGNTHSNFKRWYHFDGTDQSDQSLQNLKIKYKRGTK 186
DB 123 HLNIENNTKVTWTKFTFPGRGQKDYNIWTHNFTGIDYDE-RKNOEILEFE--GHE 179

QY 187 WDMVEVDIENGNDYLMVADIMDMHPEVINELRNMGVYVNTNLNLDGFRIDAVKHKYSY 246
DB 180 WDNVDSENNNFYLMAGADLDFSVSETVQLEKMGHWFSEMTKIDGFRDLDAIKHIDEKYF 239

QY 247 RDLWTHVRNTTGPMPFAVAFKNDLAATENYLNKTSWNHVSFDPVPLHLYNLNASNSG 306
DB 240 DKWLEQRAKQLDRKLFIVGEYWSDDLKLEYLQSSDRITQLDFVPLHFNMKKEASTN 299

QY 307 FDMRNILNGSVQKHPHATVFDVNDHDSQPEALSFVQSWFKPLAYALILTRQOGYPS 366
DB 300 FDMRTLFDHTLTASQPELSVTFVDNHDITQEQALOSWIPANFKEHAYSLILLRKKETPV 359

QY 367 FYDGYGIGTGHVPSMKSIDPLLOARQYVYAGTQHDYDHDHDIIGTWREGDSSHNSGL 426
DB 360 FWGDLYGIPSHVNPVPGDNLRTMIALRKDSBEFLRENDYFDHPDIIIGTNTLNILKIDNKEYGL 419

QY 427 ATIMSDGPGCKWYVGHKAGOVWRDITGNRSCTVINADGNGFTVNGGAVSV 483
DB 420 SCILTNKNGSKYMIIDKAYAGKYIIDLFGHREIPITLDQNGGAEFYVNDGVSVMV 476

RESULT 10
B45738
alpha-amylase (EC 3.2.1.1), cytosolic - Salmonella typhimurium
N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C;Species: Salmonella typhimurium
C;Date: 07-Apr-1994 #sequence_revision 18-Aug-1995 #text_change 18-Jun-1999
C;Accession: B45738
R;Raha, M.; Kawagishi, I.; Mueller, V.; Kihara, M.; Macnab, R.M.
J. Bacteriol. 174, 6644-6652, 1992
A;Title: Escherichia coli produces a cytoplasmic alpha-amylase, amyA.
A;Reference number: A45738; MUID:93015717
A;Molecule type: DNA
A;Accession: B45738
A;Residues: 1-494 <RAH>
A;Cross-references: GB:L01643; NID:g154043; PIDN:AAA27110.1; PID:g154045
C;Genetics:
A;Gene: amyA
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: alpha-amylase, amylioliquefaciens type; alpha-amylase core homology
C;Keywords: cytosol; glycosidase; hydrolase; polysaccharide degradation
F;202-335/Domain: alpha-amylase core homology <AMY>
F;239,265,332/Active site: His, Glu, Asp #status predicted

Query Match          38.8%; Score 1053; DB 1; Length 494;
Best Local Similarity 42.1%; Pred. No. 3.8e-64;
Matches 207; Conservative 84; Mismatches 183; Indels 18; Gaps 6;

QY 6 NGTMMQYFEHLFNDGNHNRRLDDAANKSKGITYAVWIPPAWKTSQNDVGYGAYDLYD 64
DB 3 NPTLQYFHYPPDGGKWLSELAERADGLNDIGINWVLPACKGASGGYVGYDYDLYD 62

QY 65 DLGENOKGVTRTKYGRSOLQAVTSILKNGIQVYGDVYVNNHKGADGTEMVNAVEVNR 124
DB 63 DLGEFDQKGVTRTKYGRSOLQAVTSILKNGIQVYGDVYVNNHKGADGTEMVNAVEVNR 122

QY 125 SNRNOEISGEYTIKAWTKFDPGRGNTHSNFKRWYHFDGTDQSDQSLQNLKIKYKRG-- 182
DB 123 DDRTOIDDDNIECEGWTRYTFPARAGQYSNFIDWYHCFSGIDHIENPD-EDGFIKIVNDY 181

QY 183 TCKANDWEVDIENGNDYLMVADIMDMHPEVINELRNMGVYVNTNLNLDGFRIDAVKHK 242

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[illegible]

RESULT 11

A45738

alpha-amylase (EC 3.2.1.1), cytosolic - *Escherichia coli*

N:Alternate names: 1,4-alpha-D-glucan glucanohydrolase

C:Species: *Escherichia coli*

C:Date: 07-Apr-1994 #sequence_revision 31-Oct-1997 #text_change 18-Jun-1999

C:Accession: D64956; A45738

R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.;
.A.; Rose, D.J.; Mau, B.; Shao, Y.

C:Science 277, 1453-1462, 1997

A:Title: The complete genome sequence of *Escherichia coli* K-12.

A:Reference number: A64720; MUID:97426617

A:Accession: D64956

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-495 <BLAT>

A:Cross-references: GB:AE000285; GB:U00096; NID:q1788229; PIDN:AAC74994.1;

A:Experimental source: strain K-12, substrain MG1655

R:Baba, M.; Kawagishi, I.; Mueller, V.; Kihara, M.; Macnab, R.M.

J. Bacteriol. 174, 5644-5652, 1992

A:Title: *Escherichia coli* produces a cytoplasmic alpha-amylase, amyA.

A:Reference number: A45738; MUID:93015717

A:Accession: A45738

A:Molecule type: DNA

A:Residues: 1-18, 'SS', '21-108, 'V', '110-148, 'E', '150-233, 'I', '235-495 <RAH>

A:Cross-references: GB:L01642; NID:q146021; PIDN:AAA23810.1; PID:q146023

C:Genetics:

A:Gene: amyA

C:Function:

A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic

A:Pathway: glycogen/starch degradation

C:Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core ho

C:Keywords: cytosol; glycosidase; hydrolase; polysaccharide degradation

F:202-335/domain: alpha-amylase core homology <AMY>

F:104, 204, 239/Binding site: calcium (Asn, His)

F:235, 265, 332/Active site: Asp, Glu, Asp #status predicted

Query Match	37.7%	Score 1022;	DB 1;	Length 495;
Best Local Similarity	41.1%	Pred. No. 4.8e-62;		
Matches 202; Conservative	82;	Mismatches 191;	Indels 16;	Gaps 5;

Qy	6	NTGMQVFEWHL	PDNGNNHNR	LRDDAANL	KSGLTAVW	IPPAWKGYTSQ	N-DVGYGAYDLY	64
Db	3	NPTLLQCFHWY	PEGGKLWPE	LAERADG	FDINDINM	VWLPKYGASGGY	SVGYDSDYLF	62
Qy	65	DLGFENQKGY	VTYRKYGR	SQIQAGAVT	SLKNNG	IQVYGDVVMN	HKGADGTEMYNAV	124
Db	63	DLGFDQKGS	TPTYKGDAQ	LLAAIDALK	RNDLAVLD	VVNNHKMG	ADKEALRVORNA	122

[illegible]

Query Match 37.1%; Score 1006; DB 2; Length 495;
Best Local Similarity 40.7%; Pred. No. 5.9e-61;
Matches 200; Conservative 83; Mismatches 192; Indels 1

Qy	6	NGTMQVFEWHL	PNDGNHNRRLR	DDAANLKS	KGITAV	WIPPAWKGT	SQSN-DV	GYGAYDLY	64	
Db	3	NPTLLQFHYY	PEGGKLWPEL	ARADGDFND	IGINVMWL	PPAYK	GASGGYSV	GYDSDLF	62	
Qy	65	DLGFENOKG	VTYKVT	SGTYS	LOQAVT	SLK	NNKG	IOVYGDV	VVMNHKGGADGTE	124
Db	63	DLGDFDQ	SGSIPT	KYGDV	QLLAID	ALKRND	IAVLDDV	VVMNHKGADE	KEATV	122
Qy	125	SNRQKEIS	GEYTI	EAWTK	FDPP	GGRGNT	HSFK	KRWYH	FHDGTD	182
Db	123	DDRTQID	EEICE	EGWTRY	TPPAR	AGOSY	SQFIM	DFKCF	SGIDH	181
Qy	193	TGKAWD	EVDI	ENGYD	LYAD	IDMDH	PEVIN	ELRNW	GWYVYNT	242
Db	182	TGEGNWD	QDDEL	GNFY	LMGENT	IDFR	HAHT	EEIKY	WAWMBOT	241
Qy	243	YSYTRD	WLTH	VRNTT	TGKPM	FAVE	EFKND	LAAI	ENYLNKT	302

RESULT 14

A29130

C:Species: Bacillus polymyxa

C:Date: 25-Oct-1987 #sequence_revision 03-Mar-1994 #text_change 15-Oct-1999

C:Accession: A29130; B29130; A32251; A29108

R:Rawata, T.; Nakanishi, Y.; Uozumi, N.; Sasaki, T.; Yamagata, H.; Tsukagoshi, N.; U. J. Bacteriol. 169, 1564-1570, 1987

A:Title: Cloning and nucleotide sequence of the gene coding for enzymatically active

A:Reference number: A29130; MUID:87165765

A:Accession: A29130

A:Molecule type: DNA

A:Residues: 1-936 <RAW>

A:Cross-references: GB:M15817

A:Experimental source: strain 72

A:Accession: B29130

A:Molecule type: protein

A:Residues: 36-50 <KA2>

R:Uozumi, N.; Sakurai, K.; Sasaki, T.; Takekawa, S.; Yamagata, H.; Tsukagoshi, N.; U. J. Bacteriol. 171, 375-382, 1989

A:Title: A single gene directs synthesis of a precursor protein with beta- and alpha-

A:Reference number: A32251; MUID:89123046

A:Accession: A32251

A>Status: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 937-1196 <UOZ>

A:Experimental source: strain 72

R:Rhodes, C.; Strasser, J.; Friedberg, F. Nucleic Acids Res. 15, 3934, 1987

A:Title: Sequence of an active fragment of B. polymyxa beta amylase.

A:Reference number: A29108; MUID:87231094

A:Accession: A29108

A:Molecule type: DNA

A:Residues: 'MIGL', 2-66, 'S', 68-99, 'D', '101-153, 'N', 155-176, 'Q', 178-226, 'KS', 229-329, 'S', 'K', 737-740, 'S', 742-757, 'N', 759-776 <RHO>

A:Experimental source: ATCC 8523

C:Genetics:

A:Start codon: TTG

C:Function:

A:Description: catalyzes both the hydrolysis of internal 1,4-alpha-D-glucosidic bonds

A:Pathway: glycocon/starch degradation

C:Superfamily: alpha-amylase core homology

C:Keywords: glycosidase; hydrolase; polysaccharide degradation

F:1-35/Domain: signal sequence #status predicted <SIG>

F:36-1196/Product: beta-amylase/alpha-amylase #status predicted <MAT>

F:908-1033/Domain: alpha-amylase core homology <AMY>

Query Match 11.6%; Score 315; DB 2; Length 1196;

Best Local Similarity 24.1%; Pred. No. 1.6e-13;

Matches 125; Conservative 67; Mismatches 189; Indels 138; Gaps 25;

Qy 1 HNGTNGTMMQYFEWHLPDNGHNRLRDDAANLKSIGITAVWIPPAWKGTSQNDV-GYG 59

Db 766 NYGFNSNSDQKWH-----GGDFQGIINKLDYIKNMGFTAIWTPVTMOKSEYAHGYH 821

Qy 60 AYDLTDLGEFNQGVTRFKYGRSLOQAVTSLKNGIOYGVVNMHKGADGTEWYNA 119

Db 822 TYDFY-----AVDGLHGTMDKLQELVRKAHDKNIAVWDVVVNHFG----- 862

Qy 120 VEVNRSNRNOEISGEYTTAEWTKFDF-PGRGNTHSNF-KRWYHFDD--TDWDQSRQLQ 175

Db 863 -----DFQPGNGFAKAFDKADWYHHNGDITDGDYNSNQ- 897

Qy 176 KIYKFGTKAWDEVDIENGWYDLYMTADIDMDHPEVINELRNKGWYVNTNLNDGFRI 235

Db 898 -----WK--IENG--DVAGLDLDHNFPATANELKNWIKWLLNETGIDGLRL 940

Qy 236 DAVKHIKYSYTRDLWTHVNTGCKPMFAVEFPKWNLDAAIENYLNKTSWNHVSFVDFPLHY 295

Qy 243 FVWIKWETKDFDQDANT-----FTWCFIEHGDPVAVGPDY---TRYLDAALDFPMY 991

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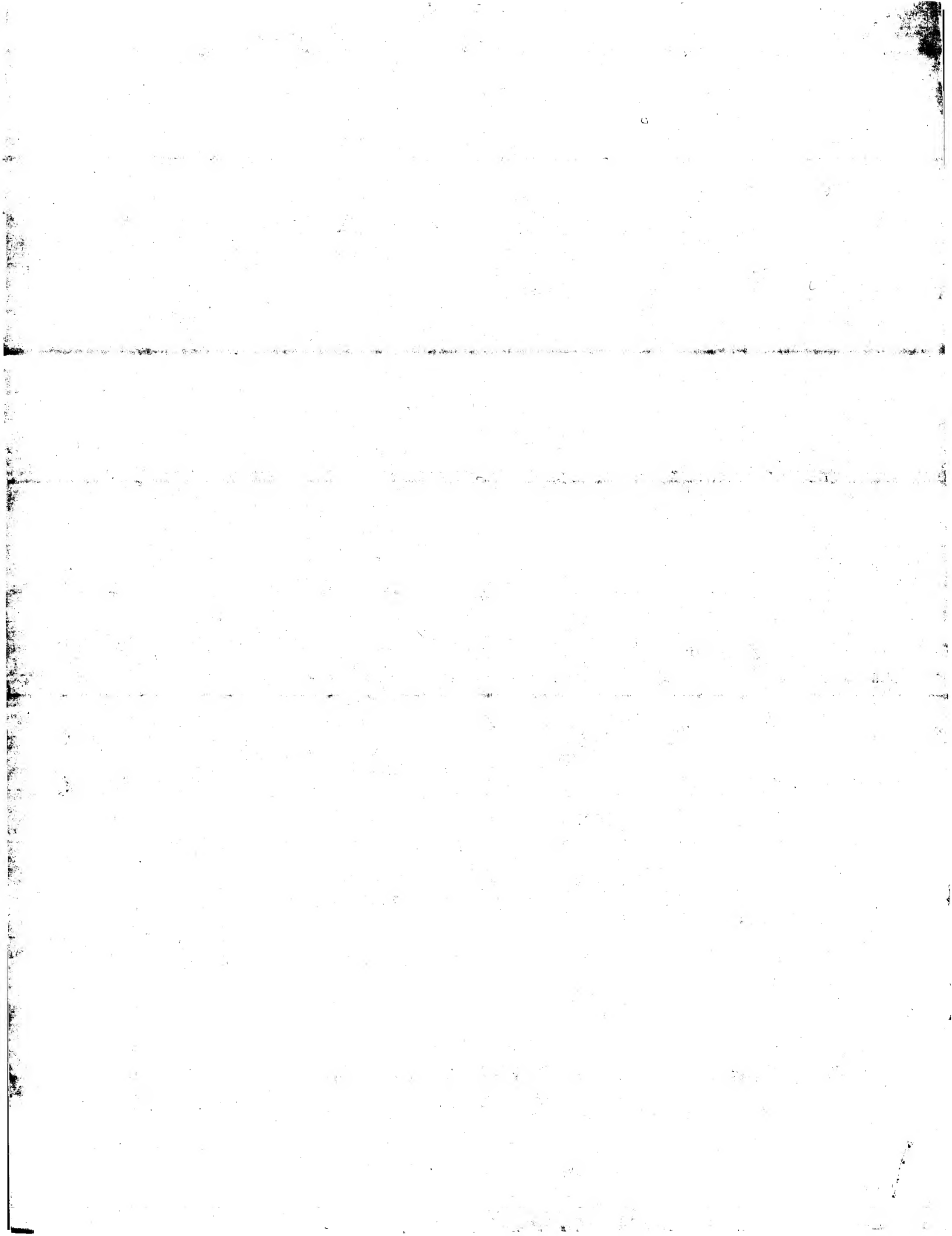
Db      408  WDDTFYAFORSYNGDEVVVMNNWSQSFTVPNIDRVANGQTLYNRMGTDKVTYVNGS 467
Qy      479  VS 480
Db      468  IT 469

Search completed: November 28, 2001, 16:59:03
Job time: 196 sec

```

R03021 15
S31478
alpha-amylase (EC 3.2.1.1) - Thermoactinomyces vulgaris
C:Species: Thermoactinomyces vulgaris
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 22-Oct-1999
C:Accession: S31478
R:Hofemeister, B.; Koenig, S.; Hoang, V.; Engel, J.; Mayer, G.; Heese, O.; Hansen, G.; Hansen, G.;
submitted to the EMBL Data Library, December 1992
A:Description: The gene amyTV coding for a non-glucoconic alpha-amylase from Thermoactino
A:Reference number: S31478
A:Accession: S31478
A:Molecule type: DNA
A:Residues: 1-482 <HOF>
A:Cross-references: EMBL:X69807; NID:g48289; PIDN:CAA49465.1; PID:g48290
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:194-319/Domain: alpha-amylase core homology <AMV>

Query Match	11.2%	Score	304.5;	DB	2;	Length	482;
Best Local Similarity	24.1%;	Pred. No.	2.5e-13;				
Matches	116;	Conservative	62;	Mismatches	171;	Indels	133;
Gaps	24;						
Qy	34	LKSGITAVWIPPAWKGTSONDV--GYGAYDLYDLGEFNQKGTVRTKYGTRSOLOQAVTSL	92				
Db	86	IKNGGTAIWITPVTMQKSANAYHYTYDFY-----SVDGHLGSMAKLQELVRAA	136				
Qy	93	KNGGIQYGVGVMMHKGAGDCTEMVNAVVRNSRNOEISGEYITIAEWTKDFDFPGRGNTH	152				
Db	137	HAKGISVMLDVVAHH-----TGDFQSPSFAPKD-----	166				
Qy	153	SNFKRWYHF--DGTDMQSRQLQNKYKFRGTCKAWDWEVDIENGNDYLYMAYADIMDH	210				
Db	167	--RADMYHHYGDQDWNQD-----W-W--VENG--DIAGLDDLQNQDN	201				
Qy	211	PEVNELRNGVWVTNTLNLDGFRIDAVKHKKYSYTRDMLTHVRNTTKCPMFAVAERPKN	270				
Db	202	PAVATELKNITAMIVQTTGVDGLRVDVTKVPKFWREF--DGAANT-----FTLGEVFHG	255				
Qy	271	DLAAIENYLNKTSNNHSVDFVPLHYLNYNASNSSGGEYFDMRNLINGSVVQ---KHPIHAVT	327				
Db	256	DPAYVGDY---TNYLDVLDPPMYITTKNV--FGQDSMRTIADRYAODYRYKKNPMTNGL	310				
Qy	328	FVDNHD-----SQPGEALESFVGSWFKPLAYALILIREQYGPSPYFYGDYIGPIPHG	378				
Db	311	FIDNHDPVREFLNEASGKPGASDWKWPQ--LKAALGFMFTTR--GIPILYQCTEQG-----	361				
Qy	379	VPSMKSITDPLQARQYAYGTCQHDYFDHDDIIGWTRGDSHPNSGLATIMSDGPGGNK	438				
Db	362	---FSGGADP--YNRDDMVFNKDKHELGYIAKLNYIR-----NTHVA---LRGTQAEK	407				
Qy	439	WM-----VYGHKHKAGQV---WRDITGN-----RSGTVTITINADGNGFETVANGA	478				



OM of: US-09-590-375-2 to: Issued_Patents_NA:* out_format : pfs
Date: Nov 28, 2001 5:38 PM
About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:

-MODEL=framet_p2n.model -DEV=xlh
-O=/cgn2_1/USPTO.spool/US09590375/runat_28112001_152038_21070/app_query.fasta_1.1092
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=rni -GAPOP=12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-XGAPOP=4.500 -XGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-FCGAPOP=6.000 -FCGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs
-NORM=ext -MINLEN=0 -MAXLEN=2000000000
-USER=US09590375 -CGN1_1_107 -NCPU=6 -ICPU=3 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPXY -WAIT -THREADS=1

Search information block:

Query: US-09-590-375-2
Query length: 485
Database: Issued_Patents_NA:*
Database sequences: 351203
Database length: 113238999
Search time (sec): 64.100000

score_list:

Sequence	Strd Orig	zScore	Escore	Len	Documentation
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/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-600-656-4		2613.00	4886.90	1.5e-264	1455
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-170-670-9		2613.00	4886.90	1.5e-264	1455
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-170-670-14		2613.00	4886.90	1.5e-264	1455
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/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-193-068-13		2613.00	4886.90	1.5e-264	1455
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-183-412-9		2613.00	4886.90	1.5e-264	1455
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-183-412-13		2613.00	4886.90	1.5e-264	1455
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-354-191A-4		2613.00	4886.90	1.5e-264	1455
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-600-908A-11		2613.00	4886.87	1.5e-264	1458
/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-683-838A-11		2613.00	4886.87	1.5e-264	1458
/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-446-803-5		2440.00	4561.40	2.0e-246	1455
/cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-861-837-5		2440.00	4561.40	2.0e-246	1455
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seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-446-803-4

seq_documentation block:

; Sequence 4, Application US/08446803
; Patent No. 5824531
; GENERAL INFORMATION:
; APPLICANT: Ottrup, Helle
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Ostergaard, Peter Rahbek
; APPLICANT: Rasmussen, Michael Dolberg
; APPLICANT: Van der Zee, Pia
; TITLE OF INVENTION: Alkaline Bacillus Amylase
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: No. 58245310 No. 5824531disk of No. 5824531th America
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,803
; FILING DATE: 01-June-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Harrington, James J.
; REGISTRATION NUMBER: 38,711
; REFERENCE/DOCKET NUMBER: 4157.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 867-0123
; TELEFAX: (212) 878-9655
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1455 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-446-803-4

alignment_scores:
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Ratio: 5.421 Gaps: 0
Percent Similarity: 99.381 Percent Identity: 95.052

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; Sequence 4, Application US/08861837
; Patent No. 5856164

GENERAL INFORMATION:
; APPLICANT: Otrup, Helle
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Ostergaard, Peter Rabbek
; APPLICANT: Rasmussen, Michael Dolberg
; APPLICANT: Van Der Zee, Pia
; TITLE OF INVENTION: Alkaline Bacillus Amylase
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 58561640 No. 5856164disk of No. 5856164th America
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/861,837
; FILING DATE:
; CLASSIFICATION: 435

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/446,803
; FILING DATE: 01-June-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Harrington, James J.
; REGISTRATION NUMBER: 38,711
; REFERENCE/DOCKET NUMBER: 4157.204-US
; TELECOMMUNICATION INFORMATION:

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; TELEPHONE: (212) 867-0123
 ; TELEFAX: (212) 878-9655
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1455 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; US-08-861-837-4

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Patent No. 6093562
GENERAL INFORMATION:
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torben Vedel
TITLE OF INVENTION: AMYLASE VARIANTS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESS: No. 60935620 No. 6093562disk of No. 6093562th America, Inc.
STREET: 405 Lexington Avenue, Suite 6400
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/600,656
FILING DATE: 13-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Landiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4318.204-US
TELEPHONE: 212 867 0123
TELEFAX: 212 867 0298
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1455 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-600-656-4

alignment_scores:
Quality: 2613.00 Length: 485
Ratio: 5.421 Gaps: 0
Percent Similarity: 99.381 Percent Identity: 95.052
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51 GCCAAATGACGGGAATCATTTGGACAGGTTGAGGGATGACGCACTAACT 100
34 euLysSerLysGlyIleThrAlaValTrpIleProProAlaTrpLysGly 50
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51 ThrSerGlnAsnAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuG 67
151 ACTTCCCAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 200
67 yCluPheAsnGlnLysGlyThrValArgThrLysTyrGlyThrArgSerG 84
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; Sequence 9, Application US/09170670
; Patent No. 6187576
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgaard-Frantzen Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 5276.200-US
; CURRENT APPLICATION NUMBER: US/09/170, 670
; CURRENT FILING DATE: 1998-10-13
; EARLIER APPLICATION NUMBER: 1172/97
; EARLIER FILING DATE: 1997-10-13
; EARLIER APPLICATION NUMBER: 60/063, 306
; EARLIER FILING DATE: 1997-10-28
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 1455
; TYPE: DNA
; ORGANISM: Bacillus sp.
US-09-170-670-9

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alignment_scores:
Quality: 2613.00      Length: 485
Ratio: 5.421          Gaps: 0
Percent Similarity: 99.381      Percent Identity: 95.052

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; Sequence 14, Application US/09170670
; Patent No. 6187576
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgaard-Frantzen Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 5276.200-US
; CURRENT APPLICATION NUMBER: US/09/170,670
; CURRENT FILING DATE: 1998-10-13
; EARLIER APPLICATION NUMBER: 1172/97
; EARLIER FILING DATE: 1997-10-13
; EARLIER APPLICATION NUMBER: 60/063,306
; EARLIER FILING DATE: 1997-10-28
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 1455
; TYPE: DNA
; ORGANISM: Bacillus sp.
US-09-170-670-14

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Ratio: 5.421          Gaps: 0
Percent Similarity: 99.381      Percent Identity: 95.052

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301 SerAsnSerGlyTyrPheAspMetArgAsnIleLeuAsnGlySerVa 317
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; Patent No. 6197565
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Kjoluff, S ren
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Andersen, Carsten
; TITLE OF INVENTION: -Amylase Variants
; FILE REFERENCE: 5709.000-US
; CURRENT APPLICATION NUMBER: US/09/193,068
; CURRENT FILING DATE: 1998-11-16
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 1455
; TYPE: DNA
; ORGANISM: Bacillus sp.
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US-09-193-068-9

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Quality: 2613.00 Length: 485
Ratio: 5.421 Gaps: 0
Percent Similarity: 99.381 Percent Identity: 95.052
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Align seg 1/1 to: US-09-193-068-9 from: 1 to: 1455

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51 GCCAATATGACGGGAATCATTTGGACAGGTTGAGGATGACGACGTAAC 100

34 eulysSerLysGlyIleThrAlaValTrpIleProProAlaTrpLysGly 50
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101 TAAAGACTAAAGGATTAACAGCTGTATGGATCCACCTGCATGGAAGGG 150

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Thu Nov 29 10:43:47 2001

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; Patent No. 6197565
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Kirulff, S ren
; APPLICANT: Bisgaard-Prantzen, Henrik
; APPLICANT: Andersen, Carsten
; TITLE OF INVENTION: -Amylase Variants
; FILE REFERENCE: 5709.000-US
; CURRENT APPLICATION NUMBER: US/09/193.068
; CURRENT FILING DATE: 1998-11-16
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 1455
; TYPE: DNA
; ORGANISM: Bacillus sp.
US-09-193-068-13
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Quality: 2613.00 Length: 485
Ratio: 5.421 Gaps: 0
Percent Similarity: 99.381 Percent Identity: 95.052
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351 AAATGCGGTAGAGTGAATCGGACCAACCCGAAACCCAGCAACCTCAGGAG 400
134 luTyrThrIleGluAlaTrpThrLysPheAspPheProGlyArgGlyAsn 150
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167 pAspGlnSerArgGlnLeuGlnAsnLysIleTyrLysPheArgGlyThrG 184
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; Sequence 9, Application US/09183412
; Patent No. 6204232
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben V.
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nissen, Torben L.
; APPLICANT: Kjaerulff, Soren
; TITLE OF INVENTION: Alpha-Amulase Mutants
; FILE REFERENCE: 5368.200-US
; CURRENT APPLICATION NUMBER: US/09/183,412
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; CURRENT FILING DATE: 1998-10-30
; EARLIER APPLICATION NUMBER: 60/064,662
; EARLIER FILING DATE: 1997-11-06
; EARLIER APPLICATION NUMBER: 60/093,234
; EARLIER FILING DATE: 1998-07-17
; EARLIER APPLICATION NUMBER: 1240/97
; EARLIER FILING DATE: 1997-10-30
; EARLIER APPLICATION NUMBER: PA 1998 00936
; EARLIER FILING DATE: 1998-07-14
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 1455
; TYPE: DNA
; ORGANISM: Bacillus
US-09-183-412-9

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Quality: 2613.00 Length: 485
Ratio: 5.421 Gaps: 0
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; Sequence 13, Application US/09183412
; Patent No. 6204232
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben V.
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nissen, Torben L.
; APPLICANT: Kjaerulff, Soren
; TITLE OF INVENTION: Alpha-Amulase Mutants
; FILE REFERENCE: 5368.200-US
; CURRENT APPLICATION NUMBER: US/09/183,412
; CURRENT FILING DATE: 1998-10-30
; EARLIER APPLICATION NUMBER: 60/064,662
; EARLIER FILING DATE: 1997-11-06
; EARLIER APPLICATION NUMBER: 60/093,234
; EARLIER FILING DATE: 1998-07-17
; EARLIER APPLICATION NUMBER: 1240/97
; EARLIER FILING DATE: 1997-10-30
; EARLIER APPLICATION NUMBER: PA 1998 00936
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 1455
; TYPE: DNA
; ORGANISM: Bacillus sp.
US-09-183-412-13

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Ratio: 5.421 Gaps: 0
Percent Similarity: 99.381 Percent Identity: 95.052

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: Sequence 4, Application US/09354191A
: Patent No. 6297038
: GENERAL INFORMATION:
: APPLICANT: Bisgard-Frantzen, Henrik
: APPLICANT: Svendsen, Allan
: APPLICANT: Borchert, Torben Vedel
: TITLE OF INVENTION: AMYLASE VARIANTS
: NUMBER OF SEQUENCES: 32
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: No. 6297038o No. 6297038disk of No. 6297038th America, Inc.
: STREET: 405 Lexington Avenue, Suite 6400
: CITY: New York
: STATE: New York
: COUNTRY: U.S.A.
: ZIP: 10174-6401
: COMPUTER READABLE FORM:
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/354,191A
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/600,656
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Lambiris, Elias J.
: REGISTRATION NUMBER: 33,728
: REFERENCE/DOCKET NUMBER: 4318.204-US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 212 867 0123
: TELEFAX: 212 867 0298
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1455 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
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alignment_scores:
  Quality: 2613.00      Length: 485
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Align seg 1/1 to: US-09-354-191A-4 from: 1 to: 1455

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; Patent No. 5989169
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisg rd-Frantzen, Henrik
; APPLICANT: Borcherdt, Torben Vedel
; TITLE OF INVENTION: A-Amylase Mutants
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 59891690 No. 5989169disk of No. 5989169th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

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; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/600,908A
 ; FILING DATE: 13-FEB-1996
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Green, Reza
 ; REGISTRATION NUMBER: 38,475
 ; REFERENCE/DOCKET NUMBER: 4394.204-US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212-867-0123
 ; TELEFAX: 212-878-9655
 ; INFORMATION FOR SEQ ID NO: 11:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1458 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; FEATURE:
 ; NAME/KEY: CDS
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 ; Sequence 11, Application US/08683838A
 ; Patent No. 6022724

GENERAL INFORMATION:
 APPLICANT: Svendsen, Allan
 APPLICANT: Bisg rd-Frantzen, Henrik
 APPLICANT: Borchert, Torben Vedel
 TITLE OF INVENTION: -Amylase Mutants
 NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:
 ADDRESSSEE: NO. 6022724O NO. 6022724disk of No. 6022724th America, Inc.
 STREET: 405 Lexington Avenue, 64th Floor
 CITY: New York
 STATE: New York
 COUNTRY: United States of America
 ZIP: 10174-6401

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/683,838A
 FILING DATE:

CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/600,908
 FILING DATE: 13-FEB-1996

ATTORNEY/AGENT INFORMATION:
 NAME: Green, Reza
 REGISTRATION NUMBER: 38,475
 REFERENCE/DOCKET NUMBER: 4394.204-US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-867-0123
 TELEFAX: 212-878-9655

INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1458 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:

NAME/KEY: CDS
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 US-08-683-838A-11

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; Patent No. 5824531
; GENERAL INFORMATION:
; APPLICANT: Otrup, Helle
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Ostergaard, Peter Rabbek
; APPLICANT: Rasmussen, Michael Dolberg
; APPLICANT: Van Der Zee, Pia
; TITLE OF INVENTION: Alkaline Bacillus Amylase
; NUMBER OF SEQUENCE: 5
; CORRESPONDENCE ADDRESSES:
; ADDRESS: No. 5824531 No. 5824531disk of No. 5824531th America
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446.803
; FILING DATE: 01-June-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Harrington, James J.
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; REGISTRATION NUMBER: 38,711
; REFERENCE/DOCKET NUMBER: 4157.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 867-0123
; TELEFAX: (212) 878-9655
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1455 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
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; Patent No. 5856164
; GENERAL INFORMATION:
; APPLICANT: Ottup, Helle
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Ostergaard, Peter Rahbek
; APPLICANT: Rasmussen, Michael Dolberg
; APPLICANT: Van Der Zee, Pia
; TITLE OF INVENTION: Alkaline Bacillus Amylase
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5856164o No. 5856164disk of No. 5856164th America
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/861,837
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/446,803
; FILING DATE: 01-June-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Harrington, James J.
; REGISTRATION NUMBER: 38,711
; REFERENCE/DOCKET NUMBER: 4157.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 867-0123
; TELEFAX: (212) 878-9655
; INFORMATION FOR SEQ ID NO: 5:
; LENGTH: 1455 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-861-837-5

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Percent Similarity: 97.732      Percent Identity: 86.598

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; Sequence 5, Application US/08600656
; Patent No. 6093562
; GENERAL INFORMATION:
; APPLICANT: Bissard-Prantzen, Henrik
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: AMYLASE VARIANTS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 60935620 No. 6093562disk of No. 6093562ch America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/600,656
; FILING DATE: 13-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4318.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 867 0298
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1455 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
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 Percent Similarity: 97.732 Percent Identity: 86.598

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PF 25-FEB-1999; 99JP-0048213.
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PR 25-FEB-1999; 99JP-0048213.
XX
PA (KAOS) KAO CORP.
XX
DR WPI; 2000-615143/59.

DR P-PSDB; AAB35714.
 XX A novel mutant alpha-amylase for use in a detergent composition -
 XX
 XX Example 1; Page 6-9; 12pp; Japanese.
 XX
 CC The present invention relates to a mutant alpha-amylase. Included in the
 CC invention are a gene encoding the mutant alpha-amylase, a vector
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 448 TGAGTTTAAACCAAAAGGAACCGTCGGTACAAAATATGGCAAGAGTC 497
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 101 GlyAspValValMetAsnHisLysGlyGlyAlaAspGlyThrGluMetVa 117
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 548 GGGGATGTCGTGATCAATCATAAAGGTGGAGCAGACGGGACAGATGGT 597
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 117 IasnAlaValGluValAsnArgSerAsnArgAsnGlnGluIleSerGlyG 134
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 134 LuTyrThrIleGluAlaTrpThrLysPheAspPheProGlyArgGlyAsn 150
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 151 ThrHisSerAsnPheLysTrpArgTrpTyrHisPheAspGlyThrAspTr 167
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 467 pGlyTrpGlyAsnPheThrValAsnGlyGlyAlaValSerValTrpVal 484
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seq_documentation_block:
ID  AAT00776 standard; DNA; 1455 BP.
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AC  AAT00776;
XX
DT  16-MAR-1996 (first entry)
XX
DE  Bacillus sp. alkaline alpha-amylase DNA.
XX
KW  Alpha-amylase; enzyme; EC-3.2.1.1; detergent; surfactant; textile;
KW  beer; starch; ss.
XX
OS  Bacillus.
XX
PN  W09526397-A1.
XX
PD  05-OCT-1995.
XX
PF  29-MAR-1995; 95WO-DK00142.
XX
PR  03-FEB-1995; 95DK-0000123.
PR  29-MAR-1994; 94DK-0000353.
PR  03-NOV-1994; 94DK-0001271.
XX
PA  (NOVO ) NOVO-NORDISK AS.
XX
PI  Bisgard-frantzen H, Ostergaard PR, Outtrup H, Rasmussen MD;
PI  Van DER ZEE P;
XX
DR  WPI: 1995-351318/45.
DR  P-PSDB; AAR81835.
XX
PT  New alkaline Bacillus alpha-amylase - used in e.g. detergent
PT  compsns. starch liquefaction, textile desizing, starch modification
PT  or beer making
XX
PS  Disclosure; Page 48-49; 65pp; English.
XX
CC  This DNA sequence may be expressed recombinantly for the production
CC  of an alpha-amylase protein. The produced protein is characterized
CC  by having a specific activity at least 25% higher than the specific
CC  activity of Termamyl at 25-55 deg C and a pH of 8-10. The enzyme
CC  can be used in detergent composition for starch liquefaction, the
CC  production of lignocellulosic materials, e.g. pulp, paper and
CC  cardboard from waste containing starch, for deinking recycled
CC  starch-coated, or starch- containing printed paper, to modify
CC  starch for papermaking, for textile desizing, and beer-making
CC  processes.
XX
SQ  Sequence 1455 BP; 461 A; 248 C; 361 G; 385 T; 0 other;

alignment_scores:
Quality: 2613.00      Length: 485
Ratio: 5.421          Gaps: 0
Percent Similarity: 99.381 Percent Identity: 95.052

alignment_block:
US-09-590-375-2 x AAT00776 ..
Align seg 1/1 to: AAT00776 from: 1 to: 1455

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1 CATCATAAATGGACAATGGTACTATGATGCAATATTCGAATGGTATT 50
|||||
17 uProAsnAspGlyAsnHisTrpAsnArgLeuArgAspAspAlaAlaAsnL 34
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51 GCCAAATGACGGGAATCATGGACAGGTGGAGGATGACGAGCTAACT 100
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34 euLysSerLysGlyIleThrAlaValTrpIleProAlaTrpLysGly 50
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67 yGluPheAsnGlnLysGlyThrValArgThrLysTyrGlyThrArgSerG 84
|||||
201 AGAGTTTAAACCAAGGGGACGCTCGTACAAAATATGGAACACCAACC 250
84 lnLeuGlnGlyAlaValThrSerLeuLysAsnGlnGlyIleGlnValTyr 100
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251 AGCTACAGGTCGGTCACTCTTTAAAAAATAACGCAATTCAGGTATAT 300
101 GlyAspValValMetAsnHisLysGlyGlyAlaAspGlyThrGluMetVa 117
|||||
301 GGTGATGTCGTATGATCATAAAGGTGGAGCAGATGGTACGGAATTTGT 350
117 lAsnAlaValGluValAsnArgSerAsnArgAsnGlnGluIleSerGlyG 134
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|||||
401 AGTATCAATAGAACGCTGGACAAAGTTTGATTTCTCTGGAAGAGAAAT 450
151 ThrHisSerAsnPheLysTrpArgTrpTyrHisPheAspGlyThrAspTr 167
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451 AACCATTCAGCTTTAAGTGGCGCTGGTATCATTTTGATGGGACAGATTG 500
167 pAspGlnSerArgGlnLeuGlnAsnLysIleTyrLysPheArgGlyThrG 184
|||||
501 GGATCAGTCAGCCAGCTTCAAAACAAATAATATAAAATTCAGGGGAACAG 550
184 lylsAlaIatrpAspTrpGluValAspIleGluAsnGlyAsnTyrAspTyr 200
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901 TCTAATAGCGGTGGTATTATGATATGAGAAATATTTAAATGGTCTCTGT 950
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1001 CTCAGCCCGGGAGCATTTGGAATCCTTTGTTCAACAATGGTTTAAACCA 1050

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seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:AAx59632

seq_documentation_block:

ID AAX59632 standard; DNA; 1455 BP.

XX AC AAX59632;

XX DT 22-JUL-1999 (first entry)

XX DE DNA encoding a termamyl-like alpha-amylase protein.

XX KW Termamyl-like; alpha-amylase; variant; washing; dishwashing;

XX KW production; sweetener; ethanol; starch; textile desizing;

XX KW starch liquefaction; saccharification process; ss.

XX OS Bacillus sp.

XX PN W09923211-Al.

XX PD 14-MAY-1999.

XX PF 30-OCT-1998; 98WO-DK00471.

XX PR 14-JUL-1998; 98DK-0000936.

XX PR 30-OCT-1997; 97DK-0001240.

XX XX (NOVO) NOVO-NORDISK AS.

XX XX Andersen C, Borchert TV, Kjaerulff S, Nielsen BR;

XX PI Nissen TL, Svendsen A;

XX XX WPI; 1999-326987/27.

XX XX New Termamyl-like alpha-amylase variants

XX PT Disclosure; Page 91-92; 115pp; English.

XX PS

XX The specification describes termamyl-like alpha-amylase variants that have altered amino acid sequences to improve properties. The variants are produced by creating one or more of the following mutations in amino acid sequence of the parent termamyl-like alpha-amylase: T141, K142, F143, D144, F145, P146, G147, R148, G149, Q174, R181, G182, D183, G184, K185, A186, W189, S193, N195, H107, K108, G109, D166, W167, D168, Q169, S170, R171, Q172, F173, F267, W268, K269, N270, D271, L272, G273, CC A274, L275, K311, E346, K385, G456, N457, K458, P459, G460, T461, V462, CC A263. The variants can be used for washing and/or dishwashing. They can also be used in the production of sweeteners and ethanol from starch, and/or for textile desizing, and in starch liquefaction and/or saccharification processes. The present sequence encodes an amylase that can function as the parent sequence in the production of the variants of the invention.

XX Sequence 1455 BP; 461 A; 248 C; 361 G; 385 T; 0 other;

alignment_scores:

Quality: 2613.00 Length: 485
Ratio: 5.421 Gaps: 0
Percent Similarity: 99.381 Percent Identity: 95.052

alignment_block:

US-09-590-375-2 x AAX59632 ..

Align seg 1/1 to: AAX59632 from: 1 to: 1455

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17 uProAsnAspGlyAsnHisTrpAsnArgLeuArgAspAlaAlaAsnL 34
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51 GCCAAATGACGGGAATCATTTGGAAACAGTTGAGGGATGACCGACTAACT 100
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84 InLeuGlnGlyAlaValThrSerLeuLysAsnAsnGlyIleGlnValTyr 100
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251 AGCTACAGGCTCGGTGACCTCTTTAAAAAATAACGGCAATTCAGGTATAT 300
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301 GGTGATGTCGTGATGATGATGATGATGATGATGATGATGATGATGATG 350
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217 uArgAsnTrpGlyValTrpTyrrThrAsnThrLeuAsnLeuAspGlyPheA 234
651 TAGAAACTGGGAGTGTGTATACGATACACACCTGACCTTGATGGATT 700
234 rgIleAspAlaValLysHisIleLysTyrrSerTyrrThrArgAspTrpLeu 250
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251 ThrHisValArgAsnThrThrGlyLysProMetPheAlaValAlaGluPh 267
751 ACACATGTGGTAAACACACAGGTAAACCAATGTTTGCAGTGGCTGAGTT 800
267 eTrpLysAsnAspLeuAlaIleGluAsnTyrrLeuAsnLysThrSerT 284
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284 rpAsnHisSerValPheAspValProLeuHisTyrrAsnLeuTyrrAsnAla 300
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1051 CTTGCATATGATGTTGTTCTGCAAGGGAACAAGTTATTCCTTCGCTATT 1100
367 eTyrrGlyAspTyrrGlyIleProThrHisGlyValProSerMetLysS 384
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XX   AAX59636;
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XX   22-JUL-1999 (first entry)
XX
XX   DNA encoding a termamyl-like alpha-amylase protein.
DE
XX
XX   Termamyl-like; alpha-amylase; variant; washing; dishwashing;
KW   production; sweetener; ethanol; starch; textile desizing;
KW   starch liquefaction; saccharification process; ss.
XX
XX   Bacillus sp.
OS
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XX   WO9923211-A1.
PN
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XX   14-MAY-1999.
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XX   (NOVO ) NOVO-NORDISK AS.
PA
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XX   Andersen C, Borchert TV, Kjaerulff S, Nielsen BR;
PI   Nissen TL, Svendsen A;
XX
XX   WPI; 1999-326987/27.
DR
XX
XX   New Termamyl-like alpha-amylase variants
PT
XX
XX   Disclosure; Page 98; 115pp; English.
PS
XX
XX   The specification describes termamyl-like alpha-amylase variants that
CC   have altered amino acid sequences to improve properties. The variants
CC   are produced by creating one or more of the following mutations in
CC   amino acid sequence of the parent termamyl-like alpha-amylase: T141,
CC   G142, F143, D144, F145, G147, R148, G149, Q174, R181, G182, D183,
CC   G184, K185, A186, W189, S193, N195, H107, K108, G109, D166, W167, D168,
CC   Q169, S170, R171, Q172, F173, F267, W268, K269, N270, D271, L272, G273,
CC   A274, L275, K311, E346, K385, G456, N457, K459, G460, T461, V462,
CC   T463. The variants can be used for washing and/or dishwashing. They can
CC   also be used in the production of sweeteners and ethanol from starch,
CC   and/or for textile desizing, and in starch liquefaction and/or
CC   saccharification processes. The present sequence encodes an amylase
CC   that can function as the parent sequence in the production of the
CC   variants of the invention.
XX
XX   Sequence 1455 BP; 461 A; 248 C; 361 G; 385 T; 0 other;
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alignment_scores:
Quality: 2613.00      Length: 485
Ratio: 5.421         Gaps: 0
Percent Similarity: 99.381 Percent Identity: 95.052

alignment_block:
US-09-590-375-2 x AAX59636 ..
Align seg 1/1 to: AAX59636 from: 1 to: 1455

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17 uProAsnAspGlyAsnHisTrpAsnArgLeuArgAspAspAlaAsnL 34
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|||||
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|||||
67 yLluPheAsnGlnLysGlyThrValArgThrLysTyrGlyThrArgSerG 84
|||||
201 AGAGTTTAAACCAAGAGGGGCGGTTCTGTACAAAATATGGAACACGCAACC 250
|||||
84 lnLeuGlnGlyAlaValThrSerLeuLysAsnAsnGlyIleGlnValTyr 100
|||||
251 AGCTACAGCGTGGGTGACCTCTTTAAATAATAACGGCATTCAGGTATAT 300
|||||
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|||||
301 GGTGATGTCGTATCAATCATATAAGGTGAGCAGATGCTACGGAATGT 350
|||||
117 lAsnAlaValGluValAsnArgSerAsnArgAsnGlnGluIleSerGlyG 134
|||||
351 AAATGCGGTAGAAGTGAATCGGAGCAACCGAAACAGGAAACCTCAGGAG 400
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134 luTyrThrIleGluAlaThrPheLysPheAspPheProGlyArgGlyAsn 150
|||||
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|||||
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|||||
901 TCTAATACGGTGGTATATGATATGAGAATAATTTAAATGGTCTGT 950
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|||||
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417 yAspSerSerHisProAsnSerGlyLeuAlaThrIleMetSerAspGlyP 434
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467 pGlyTrpGlyAsnPheThrValAsnGlyGlyAlaValSerValTrpValL 484
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1451 AGCAA 1455
seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:AAx57597
seq_documentation_block:
ID AAX57597 standard; DNA; 1455 BP.
XX
AC AAX57597;
XX
DT 16-JUL-1999 (first entry)
XX
DE Wild type Termamyl(RTM)-like alpha-amylase coding sequence #6.
XX
KW Variant; Termamyl; alpha-amylase; mutation; Bacillus; detergent;
KW dishwashing; laundry; textile; desizing; starch liquefaction;
KW sweetener; ethanol; ss.
XX
OS Bacillus sp.
XX
PN W09919467-A1.
XX
PD 22-APR-1999.
XX
PF 13-OCT-1998; 98WO-DK00444.
XX
PR 13-OCT-1997; 97DK-0001172.
XX
PA (NOVO) NOVO-NORDISK AS.
XX
PI Bisgard-Frantzen H, Borchert TV, Svendsen A;
XX
DR WPI; 1999-277632/23.
XX

PT Variant alpha-amylases - useful as detergents or for textile
 PT desizing or starch liquefaction
 XX
 PS Disclosure; Page 83-84; 93pp; English.
 XX

CC This sequence represents the coding sequence for a parent sequence
 CC used to generate new variants of a termamyl-like alpha-amylase with
 CC alpha-amylase activity. The variants comprise mutations in 2-6
 CC regions/positions relative to an alpha-amylase from either of two
 CC Bacillus species in W09526397, B. stearothermophilus, B. licheniformis,
 CC B. amyloliquefaciens or Bacillus sp. #707. The alpha-amylase variants
 CC are detergent additives for use in detergents for dishwashing, manual
 CC or automatic laundry. The variants can also be used for textile desizing
 CC or starch liquefaction (e.g. for production of sweeteners or ethanol).
 XX

SQ Sequence 1455 BP; 461 A; 248 C; 361 G; 385 T; 0 other;

alignment_scores:
 Quality: 2613.00 Length: 485
 Ratio: 5.421 Gaps: 0
 Percent Similarity: 99.381 Percent Identity: 95.052

alignment_block:
 US-09-590-375-2 x AAX57597 ..

Align seg 1/1 to: AAX57597 from: 1 to: 1455

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 1 CATCATATGGAACAAATGGTACTATGATGCAATATTTCCGAATGGTATT 50
 17 uProAsnAspGlyAsnHisTrpAsnArgLeuArgAspAspAlaAlaAsnL 34
 51 GCCAAATGACGGGAATCAATGGACAGGTGGAGGATGACCACTACT 100
 34 euLysSerLysGlyIleThrAlaValTrpIleProAlaTrpLysGly 50
 101 TAAAGAGTAAAGGGATAACAGCTGTATGATCCACCTGCATGGAAGGG 150
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 151 ACTTCCAGATGATGATAGGTATGAGCCATGATTTATATGATGCTGG 200
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 184 lLysAlaTrpAspTrpGluValAspIleGluAsnGlyAsnTyrAspTyr 200

551 CGAGCCCTGGGAGCTGGAGCTGCATACAGAGAAATGGCAACTATCACTAT 600
 201 LeuMetTyrAlaAspIleAspMetAspHisProGluValIleAsnGluLe 217
 601 CTTATGTATGAGAGCGGTGATGGATCACCAGAAAGTAATACATGAAC 650
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 651 TAGAACTGGGAGGTGGTATACGAATACACTGAACCTTGATGATTTA 700
 234 rGileAspAlaValLysHisLysTyrSerTyrThrArgAspTrpLeu 250
 701 GAATAGATGACAGTGAACATATAAATATAGCTTTACGAGAGATGGCTT 750
 251 ThrHisValArgAsnThrThrGlyLysProMetPheAlaValAlaGluPh 267
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 801 TTGGAAATATGACCTTGGTGCATTTGAAACCTATTTGAATAAACAGTT 850
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 851 GGAATCAGTCGGTGTGATGTTCTCTCCACTATAATTTGACAAATGCA 900
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 1001 CTCAGCCCGGGGAGCATTGGATCCTTTGTTCAACAATGGTTTAAACCA 1050
 351 LeuAlaTyrAlaLeuIleLeuThrArgGluGlnGlyTyrProSerValPh 367
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 384 eLysIleAspProLeuLeuGlnAlaArgGlnThrTyrAlaTyrGlyThr 400
 1151 CTAATAGACCTCTTCTGCAGGCACGTCAAACTTTTGCCTATGGTACG 1200
 401 GlnHisAspTyrPheAspHisHisAspIleIleGlyTrpThrArgGluG 417
 1201 CAGCATGATTAATTTGATCATCATGATATATATCGTTGGACAGAGAGG 1250
 417 yAspSerSerHisProAsnSerGlyLeuAlaThrIleMetSerAspGlyP 434
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1451 AGCAA 1455

seq_name: /SID52/jcgdata/geneseq/geneseqn/NA2000.DAT:AAA48480

seq_documentation_block:

ID AAA48480 standard; DNA; 1455 BP.

XX AC AAA48480;

XX DT 04-SEP-2000 (first entry)

XX DE Bacillus parent Termamyl-like alpha-amylase DNA sequence #1.

XX KW Bacillus; alpha-amylase; washing; textile desizing;

XX KW starch liquefaction; saccharification; mutein; mutant;

XX KW enzyme stability; hybrid; ss.

XX OS Bacillus sp.

XX FH Key Location/Qualifiers

XX CDS 1..1455

XX FT /*tag= a

XX FT /product= "Termamyl-like alpha-amylase"

XX FT /partial

XX FN WO200029560-A1.

XX PD 25-MAY-2000.

XX PF 16-NOV-1999; 99WO-DK00628.

XX PR 16-NOV-1998; 98DK-0001495.

XX PA (NOVO) NOVO-NORDISK AS.

XX PI Svendsen A, Kjaerulff S, Bisgard-Frantzen H, Andersen C;

XX DR WPI; 2000-387777/33.

XX DR P-PSDB; AAY99602.

XX PT Variant of parent termamyl-like alpha amylase useful for washing, textile desizing and starch liquefaction, comprising alterations in one or more solvent exposed amino acid residues .

XX PS Disclosure: Page 65-66; 80pp; English.

XX CC The present sequence encodes a parent Termamyl-like alpha-amylase from which mutants with increased stability at acidic pH, low calcium concentration and high temperatures have been derived. The sequence was isolated from a Bacillus genomic DNA library. A variant may contain mutations in one or more solvent exposed amino acid residues to increase the overall hydrophobicity of the enzyme or the overall number of methyl groups in the side chains of exposed residues may be increased. The mutations can be incorporated by site-directed mutagenesis or by random mutagenesis. As a result of their increased stability, the variants are suitable for the industrial processing of starch, i.e. starch liquefaction and saccharification. They may also be useful for washing, dishwashing and textile desizing. Hybrid alpha-amylases comprising partial amino acid sequences derived from two or more alpha-amylases have also been created in order to increase enzyme stability.

XX SQ Sequence 1455 BP; 461 A; 248 C; 361 G; 385 T; 0 other;

alignment_scores:

Quality: 2613.00

Ratio: 5.421 Length: 485

Percent Similarity: 99.381

Percent Identity: 95.052

alignment_block:

US-09-590-375-2 x AAA48480 ..

Align seg 1/1 to: AAA48480 from: 1 to: 1455

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 34 euLysSerLysGlyIleThrAlaValTrpIleProAlaTrpLysGly 50
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 51 ThrSerGlnAsnAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuG 67
 151 ACTTCCCAAGTATGATGTTATGAGCCTATGATTTATATATCTTGG 200
 67 yGluPheAsnGlnLysGlyThrValArgThrLysTyrGlyThrArgSerG 84
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 84 InLeuGlnGlyAlaValThrSerLeuLysAsnAsnGlyIleGlnValTyr 100
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 301 GGTGATGTCGTATGATCATATAAGGTGGAGCAGATGGTACGGAATTTGT 350
 117 lAsnAlaValGluValAsnArgSerAsnArgAsnGlnGluIleSerGlyG 134
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 134 LuTyrThrIleGluAlaTrpThrLysPheAspPheProGlyArgGlyAsn 150
 401 AGTATCAATAGAAAGCTGGACAAAGTTTGTCTTCTGGAAGAGGAAAT 450
 151 ThrHisSerAsnPheLysTrpArgTrpTyrHisPheAspGlyThrAspTr 167
 451 AACCATTCAGCTTTAAGTGGCGCTGTATCATTTTGTATGGGACAGATTG 500
 167 pAspGlnSerArgGlnLeuGlnAsnLysIleTyrLysPheArgGlyThrG 184
 501 GGATCAGTCACGCCAGCTTCAAAACAAAATATATAAATTCAGGGGAACAG 550
 184 lYlYsAlaTrpAspTrpGluValAspIleGluAsnGlyAsnTyrAspTyr 200
 551 GCAAGGCTGGGACTGGGAAGTCGATACAGAGAAATGGCAACTATGACTAT 600
 201 LeuMetTyrAlaAspIleAspMetAspHisProGluValIleAsnGluLe 217
 601 CTTATGTATGCACAGCTGGATATGGATCACCAGAGTAATACATGAACT 650
 217 uArgAsnTrpGlyValTrpTyrThrAsnThrLeuAsnLeuAspGlyPheA 234
 651 TAGAAATCGGGAGTGGTATACGAATACACTGAACCTTGATGGATTGA 700
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 267 eTrpLysAsnAspLeuAlaIleGluAsnTyrLeuAsnLysThrSert 284
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134 luTyrThrIleGluAlaTrpThrLysPheAspPheProGlyArgGlyAsn 150
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201 LeuMetTyrAlaAspIleAspMetAspHisProGluValIleAsnGluLe 217
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951 GGTGCAAAACATCCACACATGCGCTTACITTTTCTGTATACCATGATT 1000
334 erGlnProGlyGluAlaLeuGluSerPheValGlnSerTrpPheLysPro 350
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351 LeuAlaTyrAlaLeuIleLeuThrArgGlnGlyTyrProSerValPh 367
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1101 TTATGGGATTAATACGATATCCCAACCCATGCTGTTCGGGTATGAAT 1150
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seq_documentation_block:

ID AAX57592 standard; DNA; 1455 BP.

XX AAX57592;

XX 16-JUL-1999 (first entry)

XX Wild type Termamyl(RTM)-like alpha-amylase coding sequence #1.

XX Variant: Termamyl; alpha-amylase; mutation; Bacillus; detergent;

XX dishwashing; laundry; textile; desizing; starch liquefaction;

XX sweetener; ethanol; ss.

XX Bacillus sp.

XX WO9919467-A1.

XX 22-APR-1999.

XX 13-OCT-1998; 98WO-DK00444.

XX 13-OCT-1997; 97DK-0001172.

XX (NOVO) NOVO-NORDISK AS.

XX Bisgard-Frantzen H, Borchert TV, Svendsen A;

XX WPI; 1999-277632/23.

XX Variant alpha-amylases - useful as detergents or for textile

XX desizing or starch liquefaction

XX Disclosure; Page 76-77; 93pp; English.

CC This sequence represents the coding sequence for a parent sequence
used to generate new variants of a Termamyl-like alpha-amylase with
alpha-amylase activity. The variants comprise mutations in 2-6
regions/positions relative to an alpha-amylase from either of two
Bacillus species in WO9526397, B. stearothermophilus, B. licheniformis,
B. amyloliquefaciens or Bacillus sp. #707. The alpha-amylase variants
are detergent additives for use in detergents for dishwashing, manual
or automatic laundry. The variants can also be used for textile desizing
or starch liquefaction (e.g. for production of sweeteners or ethanol).
SQ Sequence 1455 BP; 463 A; 246 C; 361 G; 385 T; 0 other;

alignment_scores:

Quality: 2601.00

Ratio: 5.396

Length: 485

Gaps: 0

Thu Nov 29 10:43:46 2001

Percent Similarity: 99.381 Percent Identity: 94.433
alignment_block:
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Align seg 1/1 to: AAX57592 from: 1 to: 1455
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|||||
17 uProAsnAspGlyAsnHisTrpAsnArgLeuArgAspAspAlaAlaAsnL 34
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51 GCCAAATGACGGGAATCATTTGGAACAGGTGAGGGATGACGAGCTAACT 100
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34 euLysSerLysGlyLeuThrAlaValTrpProAlaTrpLysGly 50
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51 ThrSerGlnAsnAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuG 67
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151 ACTTCCAGAAATCATGTAGTTATGAGGCTATGATTTATATGATCTGG 200
|||||
67 yGluPheAsnGlnLysGlyThrValArgThrLysTyrGlyThrArgSerG 84
|||||
201 AGAGTTTAAACCAAGAGGGGACGGTTCTGACAAATATGGAACACGCAAC 250
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84 lnLeuGlnGlyAlaValThrSerLeuLysAsnAsnGlyLeuGlnValTyr 100
|||||
251 AGCTACAGGCTGGGTGACCTCTTTAAAAAATAACGGCATTCAGGTATAT 300
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101 GlyAspValValMetAsnHisLysGlyGlyAlaAspGlyThrGluMetVa 117
|||||
301 GGTGATCTGTCATGAATCAATAAGGTGGAGACAGATGTTACGGAATGT 350
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117 lAsnAlaValGluValAsnArgSerAsnArgAsnGlnGluLeuSerGlyG 134
|||||
351 AAATCGGTAGAGTGAATCGGAGCAACCCGAAACACGAGAAACCTCAGAG 400
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134 luTyrThrIleGluAlaTrpThrLysPheAspPheProGlyArgGlyAsn 150
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601 CTTATGTATGCAGACGTGGATATGATCCACCCAGAGAAATATACATGACT 650
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217 uArgAsnTrpGlyValTrpTyrThrAsnThrLeuAsnLeuAspGlyPheA 234
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651 TAGAAACTGGGAGGTGGTATACCAATATACACTGAACCTTGTGATGATT 700
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234 rGileAspAlaValLysHisIleLysTyrSerTyrThrArgAspTrpLeu 250
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701 GAATAGATGCAGTGAACATATAAATATAGCTTTACGAGAGATTGGCTT 750
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267 euTrpLysAsnAspLeuAlaIleGluAsnTyrLeuAsnLysThrSerT 284
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951 GGTCAAAACATCAACACATGCGGTACTTTTGTGATAAACCATGATT 1000
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1101 TTATGGGATTACTACGGTATCCCAACCAATGGTGTCCGGCTATGAAT 1150
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384 exLysIleAspProLeuLeuGlnAlaArgGlnThrTyrAlaTyrGlyThr 400
|||||
1151 CTAAAAATAGACCCTCTTCTGCAGGACGCTCAAACTTTTGCCTATGTTACG 1200
|||||
401 GlnHisAspTyrPheAspHisHisAspIleIleGlyTyrTrpArgGluG 417
|||||
1201 CAGCATGATTACTTTGATCATCATGATATTATCGGTGGACACAGAGGG 1250
|||||
417 yAspSerSerHisProAsnSerGlyLeuAlaThrIleMetSerAspGlyP 434
|||||
1251 AAATAGCTCCCATCCAAATTCAGGCTTGGCCACCATTTATGTCAGATGCTC 1300
|||||
434 roGlyGlyAsnLysTrpMetTyrValGlyLysHisLysAlaGlyGlnVal 450
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1301 CAGGTGGTAACAAATGGATGTATGTGGGAAAAAATAAAGCGGGACAAGTT 1350
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451 TrpArgAspIleThrGlyAsnArgSerGlyThrValThrIleAsnAlaAs 467
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1351 TGGAGAGATATTACCGGAATAGGACAGCAGCCGTCACAAATTAATGCAGA 1400
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467 pGlyTrpGlyAsnPheThrValAsnGlyGlyAlaValSerValTrpValL 484
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1401 CGGATGGGTAAATTTCTCTGTTAATGGAGGTCCTGTTTCGGTTGGGTGA 1450
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484 ySgln 485
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1451 AGCAA 1455

seq_name: /SIDS2/gcgdata/geneseq/geneseq/NA1999.DAT: AAX59633

seq_documentation_block:

ID AAX59633 standard; DNA; 1455 BP.

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PD 14-MAY-1999.
 XX 30-OCT-1998; 98WO-DK00471.
 XX 14-JUL-1998; 98DK-0000936.
 PR 30-OCT-1997; 97DK-0001240.
 XX (NOVO) NOVO-NORDISK AS.
 PA
 XX
 PI Andersen C, Borchert TV, Kjaerulff S, Nielsen BR;
 PI Nissen TL, Svendsen A;
 XX
 DR WPI; 1999-326987/27.
 XX
 XX New Termamyl-like alpha-amylase variants
 PS Disclosure; Page 92-93; 115pp; English.
 XX
 CC The specification describes termamyl-like alpha-amylase variants that
 CC have altered amino acid sequences to improve properties. The variants
 CC are produced by creating one or more of the following mutations in
 CC amino acid sequence of the parent termamyl-like alpha-amylase: T141,
 CC K142, F143, D144, F145, P146, G147, R148, G149, Q174, R181, G182, D183,
 CC G184, K185, A186, W189, S193, N195, H107, K108, G109, D166, W167, D168,
 CC Q169, S170, R171, Q172, F173, F267, W268, K269, N270, D271, L272, G273,
 CC A274, L275, K311, E346, K385, G456, N457, K458, P459, G460, T461, V462,
 CC T463. The variants can be used for washing and/or dishwashing. They can
 CC also be used in the production of sweeteners and ethanol from starch,
 CC and/or for textile desizing, and in starch liquefaction and/or
 CC saccharification processes. The present sequence encodes an amylase
 CC that can function as the parent sequence in the production of the
 CC variants of the invention.
 XX
 SQ Sequence 1455 BP; 473 A; 227 C; 352 G; 403 T; 0 other;

alignment_scores:
 Quality: 2440.00 Length: 485
 Ratio: 5.148 Gaps: 0
 Percent Similarity: 97.732 Percent Identity: 86.598

alignment_block:
 US-09-590-375-2 x AAX59633 ..
 Align seg 1/1 to: AAX59633 from: 1 to: 1455

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 51 GCCTAATGATGGGAATCACTCGATAGATTAAGAGATGATGCTAGTAATC 100
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 101 TAAGAAATAGAGGTATAACCCCTATTGGATTCCGCCCTCGCTGAAAGGG 150
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 51 ThrSerGlnAsnAspValGlyTyrGlyAlaTyrAspLeuGly 67
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 151 ACTTCGCAAAATGATGGGTATGGAGCCCTATGATCTTTATGATTAGG 200
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 84 lnLeuGlnGlyAlaValThrSerLeuLysAsnAsnGlyIleGlnValTyr 100
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 |||||
 301 GGGGATGATGATGAACCATAAAGGAGGAGCTGATGCTACAGAAACGT 350

117 lAsnAlaValGluValAsnArgSerAsnArgAsnGlnGluIleSerGlyG 134
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 351 TCTTGTCTGCGAGGTGAATCCAAATACCGGAATCAAGAAATATCTGGG 400
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 134 luTyrThrIleGluAlaTrpThrLysPheAspPheProGlyArgGlyAsn 150
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 451 ACATACTCAGACTTTAAATGGCGTTGGTATCATTTCCGATGGTAGATTG 500
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 167 pAspGlnSerArgGlnLeuGlnAsnLysIleTyrLysPheArgGlyThrG 184
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 601 TTAATGATGTCAGATGATGATGATGATGATGATGATGATGATGATGATG 650
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 217 uArgAsnTrpGlyValTrpTyrThrAsnThrLeuAsnLeuAspGlyPheA 234
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284 rPAsnHisSerValPheAspValProLeuHisTyrAsnLeuTyrAsnAla 300
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351 LeuAlaTyrAlaLeuIleLeuThrArgGluGlnGlyTyrProSerValPh 367
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1151 CCAAGATTGATCCAATCTAGAGCGCGTCAAAATTTTGACATATGGAACA 1200
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1201 CAACATGATTATTTTGACCATCATATAATATATATCGGATGGACGTGAAG 1250
417 yAspSerSerHisProAsnSerGlyLeuAlaThrIleMetSerAspGlyP 434
1251 AAATACCAACGATCCCAATTCAGGACTTGCAGACTATCATGTCGGATGGGC 1300
434 rGlyGlyAsnLysTrpMetTyrValGlyLysHisLysAlaGlyGlnVal 450
1301 CAGGGGAGAGAAATGGATGTACGTAGGCAAAATAAAGCAGGTCAGTT 1350
451 TrpArgAspIleThrGlyAsnArgSerGlyThrValThrIleAsnAlaAs 467
1351 TGGCATGACATTAACATGGAATAAACCAGGAACAGTTACGATCAATGCAGA 1400
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seq_documentation_block:

ID AAX57593 standard; DNA; 1455 BP.

XX

AC AAX57593;

XX

DT 16-JUL-1999 (first entry)

XX

DE Wild type Termamyl(RTM)-like alpha-amylase coding sequence #2.

XX Variant; Termamyl; alpha-amylase; mutation; Bacillus; detergent;

KW dishwashing; laundry; textile; desizing; starch liquefaction;

KW sweetener; ethanol; ss.

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XX
OS Bacillus sp.
XX
PN WO9919467-Al.
XX
PD 22-APR-1999.
XX
PF 13-OCT-1998; 98WO-DK00444.
XX
PR 13-OCT-1997; 97DK-0001172.
XX
PA (NOVO ) NOVO-NORDISK AS.
XX
PI Bisgaard-Frantzen H, Borchert TV, Svendsen A;
XX
DR WPI; 1999-277632/23.
XX
PT Variant alpha-amylases - useful as detergents or for textile
PT desizing or starch liquefaction
XX
PS Disclosure; Page 77-78; 93pp; English.
XX
CC This sequence represents the coding sequence for a parent sequence
CC used to generate new variants of a Termamyl-like alpha-amylase with
CC alpha-amylase activity. The variants comprise mutations in 2-6
CC regions/positions relative to an alpha-amylase from either of two
CC Bacillus species in WO9526397, B. stearothermophilus, B. licheniformis,
CC B. amyloliquefaciens or Bacillus sp. #707. The alpha-amylase variants
CC are detergent additives for use in detergents for dishwashing, manual
CC or automatic laundry. The variants can also be used for textile desizing
CC or starch liquefaction (e.g. for production of sweeteners or ethanol).
XX
SQ Sequence 1455 BP; 473 A; 227 C; 352 G; 403 T; 0 other;
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alignment_scores:

Quality: 2440.00

Ratio: 5.148

Percent Similarity: 97.732

Percent Identity: 86.598

alignment_block:

US-09-590-375-2 x AAX57593 ..

Align seg 1/1 to: AAX57593 from: 1 to: 1455

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34 euLysSerLysGlyIleThrAlaValTrpIleProProAlaTrpLysGly 50
|||||
101 TAAGAAATAGAGGTATACCCGCTATTTGGATTCCGCTCGCTGGAAAGGG 150
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|||||
151 ACTTCGCAAAATGATGGGGTATGGAGCCCTATGATCTTTATGATTAGG 200
67 yGluPheAsnGlnLysGlyThrValArgThrLysTyrGlyThrArgSerG 84
|||||
201 GGAATTTAATCAAAAGGGGACGGTTCGTACTAAGTATGGACACGTAGTC 250
84 lnLeuGlnGlyAlaValThrSerLeuLysAsnGlyIleGlnValTyr 100
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301 GGGATGTAGTATGATGAACCAATAAAGGAGGAGCTGTGCTACAGAAACGT 350
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218 |
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234 rGleAspAlaValLysHisIleLysTySerTyThrArgAspTrpLeu 250
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467 pGlyTrpGlyAsnPheThrValAsnGlyGlyAlaValSerValTrpValL 484
1401 TGGATGGCTAATTTTTCAGTAATAGGAGGATCTGTTCCATTTGGGTGA 1450
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seq_documentation_block:
ID_AA57598 standard; DNA; 1455 BP.
XX
AC_AA57598;
XX
DT 16-JUL-1999 (first entry)
XX
DE Wild type Termamyl(RTM)-like alpha-amylase coding sequence #7.
XX
KW Variant; Termamyl; alpha-amylase; mutation; Bacillus; detergent;
KW dishwashing; laundry; textile; desizing; starch liquefaction;
KW sweetener; ethanol; ss.
XX
OS Bacillus sp.
XX
PN WO9919467-A1.
XX
PD 22-APR-1999.
XX
PF 13-OCT-1998; 98WO-DK00444.
XX
PR 13-OCT-1997; 97DK-0001172.
XX
PA (NOVO ) NOVO-NORDISK AS.
XX
PI Bisgard-Frantzen H, Borchert TV, Svendsen A;
XX
WPI; 1999-277632/23.
XX
PT Variant alpha-amylases - useful as detergents or for textile
PT desizing or starch liquefaction
XX
PS Disclosure; Page 84-85; 93pp; English.
XX
CC This sequence represents the coding sequence for a parent sequence
CC used to generate new variants of a Termamyl-like alpha-amylase with
CC alpha-amylase activity. The variants comprise mutations in 2-6
CC regions/positions relative to an alpha-amylase from either of two
CC Bacillus species in WO9526397, B. stearothermophilus, B. licheniformis,
CC B. amyloliquefaciens or Bacillus sp. #707. The alpha-amylase variants
CC are detergent additives for use in detergents for dishwashing, manual
CC or automatic laundry. The variants can also be used for textile desizing
CC or starch liquefaction (e.g. for production of sweeteners or ethanol).
XX
SQ Sequence 1455 BP; 473 A; 227 C; 352 G; 403 T; 0 other;
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alignment_scores:
Quality: 2440.00      Length: 485
Ratio: 5.148          Gaps: 0
Percent Similarity: 97.732 Percent Identity: 86.598
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alignment_block:
US-09-590-375-2 x AAX57598 ..
Align seg 1/1 to: AAX57598 from: 1 to: 1455

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51  GCCTAATGATGGGAATCAGTGAATAGATTAAGAGATGCTAGTAATC 100
34  euLysSerLysGlyIleThrAlaValTrpIleProProAlaTrpLysGly 50
101  TAAGAATAGAGGTATACCCGCTATTTGGATTCCGCCCTGCCGCGAAGGG 150
51  ThrSerGlnAsnAspValGlyTyrGlyAlaTyrAspLeuGlu 67
151  ACTTCGCAAAATGATGTGGGTATGGAGCCTATGATCTTTATGATTTAGG 200
67  yGluPheAsnGlnLysGlyThrValArgThrLysTyrGlyThrArgSerG 84
201  GGAATTTAATCAAAAGGGGCGGTCTGCTACTAAGTATGGGACAGTAGTC 250
84  lnLeuGlnGlyAlaValThrSerLeuLysAsnAsnGlyIleGlnValTyr 100
251  AATTGGAGTCTGCCATCCATGCTTTAAGAATAATGGCGTTCAAGTTAT 300
101  GlyAspValValMetAsnHisLysGlyGlyAlaAspGlyThrGluMetVa 117
301  GGGGATGATGATGATGAACCAATAAAGGAGGAGCTGATGATACAGAAAACGT 350
117  lasAlaValGluValAsnArgSerAsnArgAsnGlnLysSerGlyG 134
351  TCTTGCTGTCGAGGTGAATCCAAATACCGGAATCAAGAAATATCTGGGG 400
134  luTyrThrIleGluAlaTrpThrLysPheAspPheProGlyArgGlyAsn 150
401  ACTACAAATGAGCGTGGACTAAGTTGATTTCCAGGAGGGGTAAT 450
151  ThrHisSerAsnPheLysTrpArgTrpThrHisPheAspGlyThrAspTr 167
451  ACATACTCAGACTTTAAATGCGTGTGGTATCATTTCCGATGCTGATAGT 500
167  pasGlnSerArgGlnLeuGlnAsnLysIleTyrLysPheArgGlyThrG 184
501  GGATCAATCAGCAATTCCAAAATCGTATCTACAAATTCGAGGTGATG 550
184  lyLysAlaTrpAspTrpGluValAspIleGluAsnGlyAsnTyrAspTyr 200
551  GTAAGGATGGGATGGGAAGTACATTCGGAATAATGGAAATATGATAT 600
201  LeuMetTyrAlaAspIleAspMetAspHisProGluValIleAsnGluLe 217
601  TTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 650
217  uArgAsnTrpGlyValTrpThrAsnThrLeuAsnLeuAspGlyPheA 234
651  TAGAAGATGGGGAATGGTATACAAATACATTAATCTTATGATGATTTA 700
234  rgIleAspAlaValLysHisIleLysTyrSerTyrThrArgAspTrpLeu 250
701  GGATCGATGGGTGACGATATTAATATAGCTTTACACGCTGATGGTTG 750
251  ThrHisValArgAsnThrThrGlyLysProMetPheAlaValAlaGluPh 267
751  ACCCATGTAGAAAACGCAACGGGAAAAAATGTTGCTGTGCTGAAT 800
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901  TCAATAGTAGGAGCAACTATGACATGGCAAAACTCTTATATGAAGCGT 950
317  lValGlnLysHisProIleHisAlaValThrPheValAspAsnHisAsps 334
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334  erGlnProGlyGluAlaLeuGluSerPheValGlnSerTrpPheLysPro 350
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351  LeuAlaTyrAlaLeuIleLeuThrArgGluGlnGlyTyrProSerValPh 367
1051  CTTGCTTATGCGCTTATTTTAAACAAGAGAACACAGGCTATCCCTCTGCTT 1100
367  eTyrGlyAspTyrTyrGlyIleProThrHisGlyValProSerMetLys 384
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401  GlnHisAspTyrPheAspHisHisAspIleIleGlyTrpThrArgGluG 417
1201  CAACATGATTATTTTGACCATCATATATAATCGGATGGACACGTGAAG 1250
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XX
AC AAA48481;
XX
DT 04-SEP-2000 (first entry)
XX
DE Bacillus parent Termamyl-like alpha-amylase DNA sequence #2.
XX
KW Bacillus: alpha-amylase; washing; textile desizing;
KW starch liquefaction; saccharification; mutein; mutant;
KW enzyme stability; hybrid; ss.
XX
OS Bacillus sp.
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FT XX /partial

PN WO200029560-A1.

XX PD 25-MAY-2000.

XX PF 16-NOV-1999; 99WO-DK00628.

XX PR 16-NOV-1998; 98DK-0001495.

XX PA (NOVO) NOVO-NORDISK AS.

XX PI Svendsen A, Kjaerulff S, Bisgard-Frantzen H, Andersen C;

XX DR WPI: 2000-387777/33.

XX DR P-PSDB; AAY99603.

XX Variant of parent termamyl-like alpha amylase useful for washing,
PT textile desizing and starch liquefaction, comprising alterations in one
PT or more solvent exposed amino acid residues

XX PS Disclosure; Page 66-67; 80pp; English.

XX The present sequence encodes a parent Termamyl-like alpha-amylase
CC from which mutants with increased stability at acidic pH, low calcium
CC concentration and high temperatures have been derived. The sequence was
CC isolated from a Bacillus genomic DNA library. A variant may contain
CC mutations in one or more solvent exposed amino acid residues to increase
CC the overall hydrophobicity of the enzyme or the overall number of
CC methyl groups in the side chains of exposed residues may be increased.
CC The mutations can be incorporated by site-directed mutagenesis or by
CC random mutagenesis. As a result of their increased stability, the
CC variants are suitable for the industrial processing of starch, i.e.
CC starch liquefaction and saccharification. They may also be useful for
CC washing, dishwashing and textile desizing. Hybrid alpha-amylases
CC comprising partial amino acid sequences derived from two or more
CC alpha-amylases have also been created in order to increase enzyme
CC stability.

XX SQ Sequence 1455 BP; 473 A; 227 C; 352 G; 403 T; 0 other;

alignment_scores:

Quality: 2440.00 Length: 485
Ratio: 5.148 Gaps: 0
Percent Similarity: 97.732 Percent Identity: 86.598

alignment_block:

US-09-590-375-2 x AAA48481 ..

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1 CATCATATGGGCAAAATGGGACGATGATGCAATCTTTGAATGGCACTT 50

17 uProAsnAspGlyAsnHisTrpAsnArgLeuArgAspAspAlaAsnL 34

51 GCCTAATGATGGGAATCACTGGGAATAGATTAAGACATGATGCTAGTAATC 100

34 euLysSerLysGlyIleThrAlaValTrpIleProAlaTrpLysGly 50

101 TAGAAATAGAGTATAACCGCTATTTGGATCCGCTCCCTGGGAAGGG 150

51 ThrSerGlnAsnAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuG 67

151 ACTTCCCAATGATGGGATGGGATGGAGCTATGATCTTTATGATTAGG 200

67 yGluPheAsnGlnLysGlyThrValArgThrLysTyrGlyThrArgSerG 84

201 GGAATTTAATCAAAAGGGACGGTTTCGTACTAAGTATGGACACAGTAGTC 250

84 lntLeuGlnGlyAlaValThrSerLeuLysAsnGlyIleGlnValTyr 100

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401 ACTACACAATTCAGGCTTGGACTAAGTTTGATTTTCCAGGGAGGGTAAT 450
151 ThrHisSerAsnPheLysTrpArgTrpTyrHisPheAspGlyThrAspTr 167
451 ACATACTCAGACTTTAATGGCGTTGGTATCATTTCCGATGGTGTAGATTG 500
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501 GCATCAATCAGCACAAATCCAAAATCGTATCTACAAATTCGAGGTGATG 550
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551 GTAAGGCATGGGATGGGAAGTAGATTTCGAAAATGGAAATTTATGATTAT 600
201 LeuMetTyrAlaAspIleAspMetAspHisProGluValIleAsnGluLe 217
601 TTAATGTATGAGATGATAGATGATGATCGGAGGTAGTAATAGAGCT 650
217 uArgAsnTrpGlyValTrpTyrThrAsnThrLeuAsnLeuAspGlyPheA 234
651 TAGAAGATGGGAGAGATGGTATACAAATACATTAATCTTGATGATTTA 700
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701 GGATCGATCGGTGAAGCATATTAATATAGCTTTACACGCTGATGGTTG 750
251 ThrHisValArgAsnThrThrGlyLysProMetPheAlaValAlaGluPh 267
751 ACCCATGTAAGAAACGCAACGGAAGAAATGTTGCTGTTGCTGAATT 800
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801 TTGGAAAATGATTTAGTGGCTTGGAGAACATTTAAATAAAACAACT 850
284 rpAsnHisSerValPheAspValProLeuHisTyrAsnLeuTyrAsnAla 300
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351 LeuAlaTyrAlaLeuIleLeuThrArgGluGlnGlyTyrProSerValPh 367
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367 eTyrGlyAspTyrTyrGlyIleProThrHisGlyValProSerMetLys 384
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384 exLysIleAspProLeuLeuGlnAlaArgGlnThrTyrAlaTyrGlyThr 400
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ID AAA48486 standard; DNA; 1455 BP.

XX AC AAA48486;

XX DT 04-SEP-2000 (first entry)

XX DE Bacillus Termamyl-like alpha-amylase DNA sequence #4.

XX KW Bacillus; alpha-amylase; washing; textile desizing;
 KW starch liquefaction; saccharification; mutein; mutant;
 KW enzyme stability; hybrid; ss.
 XX OS Bacillus sp.

XX FH Key

FT CDS Location/Qualifiers

FT 1..1455

FT /*tag= a

FT /product= "Termamyl-like alpha-amylase"

FT /partial

XX PN WO200029560-A1.

XX PD 25-MAY-2000.

XX PF 16-NOV-1999; 99WO-DK00628.

XX PR 16-NOV-1998; 98DK-0001495.

XX PA (NOVO) NOVO-NORDISK AS.

XX PI Svendsen A, Kjaerulff S, Bisgard-Frantzen H, Andersen C;

XX DR WPI; 2000-387777/3.

XX DR P-PSDB; AAY99609.

XX PT Variant of parent termamyl-like alpha amylase useful for washing,
 PT textile desizing and starch liquefaction, comprising alterations in one
 PT or more solvent exposed amino acid residues -
 XX Disclosure; Page 70-71; 80pp; English.

XX PS The present sequence encodes a parent alpha-amylase from which mutants

CC with increased stability at acidic pH, low calcium concentration and high
 CC temperatures have been derived. The sequence was isolated from a Bacillus

CC genomic DNA library. A variant may contain mutations in one or more
 CC solvent exposed amino acid residues to increase the overall
 CC hydrophobicity of the enzyme or the overall number of methyl groups in
 CC the side chains of exposed residues may be increased. The mutations can
 CC be incorporated by site-directed mutagenesis or by random mutagenesis. As
 CC a result of their increased stability, the variants are suitable for the
 CC industrial processing of starch, i.e. starch liquefaction and
 CC saccharification. They may also be useful for washing, dishwashing and
 CC textile desizing. Hybrid alpha-amylases comprising partial amino acid
 CC sequences derived from two or more alpha-amylases have also been created
 CC in order to increase enzyme stability.
 XX
 SQ Sequence 1455 BP; 473 A; 227 C; 352 G; 403 T; 0 other;

alignment_scores:

Quality: 2440.00 Length: 485
 Ratio: 5.148 Gaps: 0
 Percent Similarity: 97.732 Percent Identity: 86.598

alignment_block:

US-09-590-375-2 x AAA48486

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 17 uProAsnAspGlyAsnHisTrpAsnArgLeuArgAspAlaAlaAsnL 34
 51 GCCTAATGATGGGAATCACTGGAATAGATTAAAGAGATGATCTAGTAATC 100
 34 euLysSerLysGlyIleThrAlaValTrpIleProProAlaTrpLysGly 50
 101 TAGAAATAGAGGTATAACCGCTATTTCGATTCCGCTCGCTGGAAGGG 150
 51 ThrSerGlnAsnAspValGlyTyrGlyValatyrAspLeuTyrAspLeuG1 67
 151 ACITCGCAAAATGATGTGGGTATGGAGCTATGATCTTTATGATTAGG 200
 67 yGluPheAsnGlnLysGlyThrValArgThrLysTyrGlyThrArgSerG 84
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 84 lnLeuGlnGlyAlaValThrSerLeuLysAsnAsnGlyIleGlnValTyr 100
 251 AATTGGAGTCTGCCATCCATGCTTTAAAGAAATAATGGCGTTCAAGTTAT 300
 101 GlyAspValValMetAsnHisLysGlyAlaAspGlyThrGluMetVa 117
 301 GGGATCTAGTGTAGTGAACCATAAAGGAGGAGCTCATGCTACAGAAACGT 350
 117 lAsnAlaValGluValAsnArgSerAsnArgAsnGlnGluIleSerGlyG 134
 351 TCTTGTCTCGAGGTGAATCCAAATAACCGGAATCAAGAAATATCTGGGG 400
 134 luTyrThrIleGluAlaTrpThrLysPheAspPheProGlyArgGlyAsn 150
 401 ACTACAAATTTAGGCTTGGACTAAGTTTGTATTTCCAGGGAGGGGTAAT 450
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 451 ACATACCTACAGACTTTAAATGGCGTTGGTATCATTTCCGATGGTAGATTG 500
 167 pAspGlnSerArgGlnLeuGlnAsnLysIleTyrLysPheArgGlyThrG 184
 501 GGATCAATCAGCACATTCGAAATCGTATCTACAAATTCGAGGTGATG 550
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Date: Nov 28, 2001 6:27 PM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 CompuGen Ltd.

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sp.
E12445

ACCESSION E12445

VERSION E12445.1 GI:3251278

KEYWORDS JP 1996336392-A/1.

SOURCE Bacillus sp.

ORGANISM Bacillus sp.

REFERENCE Bacteria: Firmicutes; Bacillus/Clostridium group;

Bacillus/Staphylococcus group; Bacillus.

1 (bases 1 to 1776)

AUTHORS Hatada,Y., Ozaki,K., Ara,K., Kawai,S. and Ito,S.

TITLE LIQUEFIED-TYPE ALKALI ALPHA-AMYLASE GENE

JOURNAL Patent: JP 1996336392-A 1 24-DEC-1996;

COMMENT KAO CORP

OS Bacillus sp.

PN JP 1996336392-A/1

PD 24-DEC-1996

PF 14-JUN-1995 JP 1995147257

PI HATADA YUJI, OZAKI KATSUYA, ARA KATSUTOSHI, KAWAI SHUJI, PI

ITO SUSUMU

PC C12N15/09,C12N9/28;

CC strandedness: Double;

CC topology: Linear;

CC hypothetical: No;

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Location/Qualifiers

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DEFINITION Bacillus sp. gene for amylase, complete cds.
ACCESSION AB008763
VERSION AB008763.1 GI:3445479
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ORGANISM Bacillus sp.
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
REFERENCE 1 (bases 1 to 1786)
AUTHORS Hatada,Y.
TITLE Direct Submission
JOURNAL Submitted (10-NOV-1997) to the DDBJ/EMBL/GenBank databases. Yuji
Akabane, Ichikai, Haga-gun, Tochigi 321-3497, Japan
(Tel.:0285-68-7400, Fax:0285-68-7403)
REFERENCE 2 (bases 1 to 1786)
AUTHORS Igarashi,K., Hatada,Y., Ikawa,K., Araki,H., Ozawa,T., Kobayashi,T.,
Ozaki,K. and Ito,S.
TITLE Improved thermostability of a Bacillus alpha-amylase by deletion of
an arginine-glycine residue is caused by enhanced calcium binding
JOURNAL Biochem. Res. Commun. 248 (2), 372-377 (1998)
MEDLINE 98342096

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Quality: 2713.00      Length: 485
Ratio: 5.594          Gaps: 0
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LOCUS AR027254

DEFINITION Sequence 4 from patent US 5856164.

ACCESSION AR027254

VERSION AR027254.1 GI:5938094

KEYWORDS

SOURCE

ORGANISM

Unclassified.

REFERENCE

1 (bases 1 to 1455)

Outtrup,H., Bisg,ang.rd-Frantzen,H., stergaard,P.Rahbek,

Rasmussen,M.Dolberg and Van Der Zee,P.

TITLE Alkaline bacillus amylase

JOURNAL Patent: US 5856164-A 4 05-JAN-1999;

FEATURES

Location/Qualifiers

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ACCESSION AR049517

VERSION AR049517.1 GI:6005556

KEYWORDS

SOURCE

ORGANISM

REFERENCE

1 (bases 1 to 1455)

Outtrup,H., Blsg,ang.rd-Frantzen,H., stergaard,P. Rahbek,

Rasmussen,M.Dolberg and Van der Zee,P.

Alkaline bacillus amylase

JOURNAL Patent: US 5824531-A 4 20-OCT-1998;

FEATURES

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Location/Qualifiers

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seq_documentation_block: 1455 bp DNA PAT 14-FEB-2001
LOCUS AR104348

DEFINITION Sequence 4 from patent US 6093562.

ACCESSION AR104348

VERSION AR104348.1 GI:12817056

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE Bisq.ang.rd-Prantzen,H., Svendsen,A. and Borchert,T.Vedel.

JOURNAL Patent: US 6093562-A 4 25-JUL-2000;

FEATURES

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/organism="unknown"

BASE COUNT 461 a 248 c 361 g 385 t

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Quality: 2613.00 Length: 485

Ratio: 5.421 Gaps: 0

Percent Similarity: 99.381 Percent Identity: 95.052

alignment_block:

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seq_documentation_block: AR129912 1455 bp DNA PAT 16-MAY-2001

DEFINITION Sequence 9 from patent US 6187576.

ACCESSION AR129912

VERSION AR129912.1 GI:14117809

KEYWORDS Unknown.

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 1455)

AUTHORS Svendsen,A., Borchert,T., Vedel and Bisg.ang.rd-Frantzen,H.

TITLE .alpha.-amylase mutants

JOURNAL Patent: US 6187576-A 9 13-FEB-2001;

FEATURES Location/Qualifiers

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/organism="unknown"

BASE COUNT 461 a 248 c 361 g 385 t

ORIGIN

alignment_scores:

Quality: 2613.00 Length: 485

Ratio: 5.421 Gaps: 0

Percent Similarity: 99.381 Percent Identity: 95.052

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DEFINITION Sequence 14 from patent US 6187576.
ACCESSION AR129917
VERSION AR129917.1 GI:14117814
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1455)
AUTHORS Svendsen,A., Borchert,T.Vedel and Bisg.ang.rd-Frantzen,H.
TITLE - .alpha.-amylase mutants
JOURNAL Patent: US 6187576-A 14 13-FEB-2001;
FEATURES
Location/Qualifiers
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BASE COUNT 461 a 248 c 361 g 385 t
ORIGIN

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Ratio: 5.421 Gaps: 0
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LOCUS AR137883 Sequence 9 from patent US 6197565.

ACCESSION AR137883

VERSION AR137883.1 GI:14479392

KEYWORDS

SOURCE

ORGANISM

Unclassified.

REFERENCE 1 (bases 1 to 1455)

AUTHORS Svendsen,A., Kjaerulff,S., Bisgaard-Frantzen,H. and Andersen,C.

TITLE .alpha.-Amylase variants

JOURNAL Patent: US 6197565-A 9 06-MAR-2001;

FEATURES

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ORIGIN

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Ratio: 5.421 Gaps: 0

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LOCUS ARL37887
DEFINITION Sequence 13 from patent US 6197565.
ACCESSION ARL37887
VERSION ARL37887.1 GI:14479396
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE
1 (bases 1 to 1455)
AUTHORS Svendsen,A., Kjaerulf,S., Bisgaard-Frantzen,H. and Andersen,C.
TITLE -alpha.-Amylase variants
JOURNAL Patent: US 6197565-A 13 06-MAR-2001;
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BASE COUNT 461 a 248 c 361 g 385 t
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Align seg 1/1 to: ARL37887 from: 1 to: 1455

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ACCESSION	AR143213		
VERSION	AR143213.1	GI:15104499	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified		
AUTHORS	1 (bases 1 to 1455)		
TITLE	Borchert,T.Vedel, Svendsen,A., Andersen,C., Nielsen,B., Nissen,T.Lauesgaard and Kj.ae buttet.ruliff,Sslashedren.		
JOURNAL	.alpha.-amlase mutants		
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BASE COUNT	461 a	248 c	361 g 385 t

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LOCUS AR143217 1455 bp DNA PAT 08-AUG-2001

DEFINITION Sequence 13 from patent US 6204232.

ACCESSION AR143217

VERSION AR143217.1 GI:15104503

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 1455)

-AUTHORS Borchert,T.Vedel., Svendsen,A., Andersen,C., Nielsen,B.,

Nissen,T.Lauesgaard and Kj.ae butted.rulff,sslashedren.
.alpha.-amlase mutants
JOURNAL Patent: US 6204232-A 13 20-MAR-2001;
FEATURES Location/Qualifiers
source 1..1455
BASE COUNT 461 a 248 c 361 g 385 t
ORIGIN

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LOCUS AR087556
DEFINITION Sequence 11 from patent US 5989169.
ACCESSION AR087556

VERSION AR087556.1 GI:10014319
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1458)
AUTHORS Svendsen,A., Bisg,ang.rd-Frantzen,H. and Borchert,T.Vedel.
TITLE .alpha.-amylase mutants
JOURNAL Patent: US 5989169-A 11 23-NOV-1999;
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LOCUS AR027255 Sequence 5 from patent US 5856164.
DEFINITION AR027255
ACCESSION AR027255
VERSION AR027255.1 GI:5938095
KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 1455)

AUTHORS Outtrup,H., Bisq,ang.rd-Frantzen,H., stergaard,P.Rahbek,

Rasmussen,M.Dolberg and Van Der Zee,P.

TITLE Alkaline bacillus amylase

JOURNAL Patent: US 5856164-A 5 05-JAN-1999;

FEATURES Location/Qualifiers

source 1..1455

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ORIGIN

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Percent Similarity: 97.732 Percent Identity: 86.598

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seq_documentation_block: 1455 bp DNA PAT 29-SEP-1999
LOCUS AR049518 Sequence 5 from patent US 5824531.
DEFINITION AR049518
ACCESSION AR049518
VERSION AR049518.1 GI:6005557
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1455)
AUTHORS Outtrup,H., Bisg,ang.rd-Frantzen,H., stergaard,P.Rahbek,
Rasmussen,M.Dolberg and Van der Zee,P.
TITLE Alkaline bacillus amylase
JOURNAL Patent: US 5824531-A 5 20-OCT-1998;
FEATURES
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DEFINITION Sequence 5 from patent US 6093562.
ACCESSION AR104349
VERSION AR104349.1 GI:12817057
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 1455)
AUTHORS Bisg.ang.rd.Frantzen,H., Svendsen,A. and Borchert,T.Vedel.
TITLE Amylase variants
JOURNAL Patent: US 6093562-A 5 25-JUL-2000;
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301 SerAsnSerGlyGlyTyrPheAspMetArgAsnIleLeuAsnGlySerVa 317
901 TCAAAATAGTGGAGCAACTATGACATGSCAAAACCTTCTTAATGGAACGGT 950
317 ValGlnLysHisProIleHisAlaValThrPheValAspAsnHisAspS 334
951 TGTTCAAAAGCATCCAAATGCATGCGTAACCTTTTGTGGATAATCACGATT 1000
334 eGlnProGlyGluAlaLeuGluSerPheValGlnSerTrpPheLysPro 350
1001 CTCACCTGGGGATCATTAAGATCATTTGTCAAGAATGGTTTAAGCCA 1050
351 LeuAlaTyrAlaLeuIleLeuThrArgGluGlnGlyTyrProSerValPh 367
1051 CTTGCTTATGCGCTTATTTTAAACAGAACCAAGGCTATCCCTCTGTCCT 1100
367 eTyrgLysPtyrTyrgIleProThrHisGlyValProSerMetLysS 384
1101 CTATGGTGACCTATATGAAATCCAAACATATGTCCTCCAGCAATGAAG 1150
384 eLysIleAspProLeuLeuGlnAlaArgGlnThrTyrAlaTyrgLysThr 400
1151 CCAACATGATTCATCTTAGAGGCGCTCAAAATTTTGCATATGGAAACA 1200
401 GlnHisAspTyrPheAspHisHisAspIleGlyTrpThrArgGluGl 417
1201 CAACATGATTTATTTGACCATCATTAATATATCCGATGCAGACGTGAAG 1250

417 yAspSerSerHisProAsnSerGlyLeuAlaThrIleMetSerAspGlyp 434
 1251 AAATACCAAGCATCCCAATTCAGGACTTGCAGCTATCATGTCGGATGGC 1300
 434 roGlyGlyAsnLysTrpMetTrpValGlyLysHisLysAlaGlyGlnVal 450
 1301 CAGGGGAGAGAAATGGATGTACGTAGGGCAAAATAAAGCAGGTCAAGTT 1350
 451 TrpArgAspIleThrGlyAsnArgSerGlyThrValThrIleAsnAlaAs 467
 1351 TGGCATGACATAACTTGGAAATAAACCAGGAACAGTTCAGCATCAATGCAGA 1400
 467 pGlyTrpGlyAsnPheThrValAsnGlyGlyAlaValSerValTrpValL 484
 1401 TGGATGGCGTAATTTTTCAGTAAATGGAGGATCTGTTTCCATTTGGGTGA 1450
 484 ysGln 485
 1451 AACGA 1455

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: November 28, 2001, 16:58:32 ; Search time 19.44 Seconds
(without alignments)
561.425 Million cell updates/sec

Title: US-09-590-375-2

Perfect score: 2713

Sequence: 1 HHNGTNGTMMQYFEWHLPND.....ADGNGFTVNGCAVSVMVK 485

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*

2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2613	96.3	485	2	US-08-446-803-1
2	2613	96.3	485	2	US-08-861-837-1
3	2613	96.3	485	2	US-08-600-908A-12
4	2613	96.3	485	3	US-08-683-838A-12
5	2613	96.3	485	3	US-08-600-656-1
6	2613	96.3	485	4	US-09-170-670-1
7	2613	96.3	485	4	US-09-170-670-7
8	2613	96.3	485	4	US-09-193-068-1
9	2613	96.3	485	4	US-09-193-068-7
10	2613	96.3	485	4	US-09-183-412-1
11	2613	96.3	485	4	US-09-183-412-7
12	2613	96.3	485	4	US-09-354-191A-1
13	2609	96.2	485	4	US-09-264-097-7
14	2440	89.9	485	2	US-08-446-803-2
15	2440	89.9	485	2	US-08-861-837-2
16	2440	89.9	485	3	US-08-600-656-2
17	2440	89.9	485	4	US-09-170-670-2
18	2440	89.9	485	4	US-09-170-670-8
19	2440	89.9	485	4	US-09-193-068-2
20	2440	89.9	485	4	US-09-193-068-8
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23	2440	89.9	485	4	US-09-264-097-5
24	2440	89.9	485	4	US-09-354-191A-2
25	2410	88.8	485	3	US-08-600-656-7
26	2410	88.8	485	4	US-09-170-670-6
27	2410	88.8	485	4	US-09-193-068-6

28	2410	88.8	485	4	US-09-183-412-6
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34	1910.5	70.4	549	1	US-08-459-610-6
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39	1909	70.4	483	1	US-08-468-700-34
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42	1909	70.4	483	2	US-08-704-706A-34
43	1909	70.4	483	3	US-08-890-383-3
44	1909	70.4	483	3	US-08-914-679A-3
45	1909	70.4	483	4	US-09-182-859-2

ALIGNMENTS

RESULT 1
US-08-446-803-1
; Sequence 1, Application US/08446803
; Patent No. 5824531
; GENERAL INFORMATION:
; APPLICANT: Otrup, Helle
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Ostergaard, Peter Rahbek
; APPLICANT: Rasmussen, Michael Dolberg
; APPLICANT: Van Der Zee, Pia
; TITLE OF INVENTION: Alkaline Bacillus Amylase
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5824531o No. 5824531disk of No. 5824531th America.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,803
; FILING DATE: 01-June-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Harrington, James J.
; REGISTRATION NUMBER: 38,711
; REFERENCE/DOCKET NUMBER: 4157.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 867-0123
; TELEFAX: (212) 878-9655
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 485 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-446-803-1

Query Match 96.3%; Score 2613; DB 2; Length 485;

Best Local Similarity 95.1%; Pred. No. 2.7e-223;
Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

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61	Db	YDLYDLGEFNQKQVTRTKYGTBSQLQGAVTSLKNNINGIQVYGDVVMNHKGGADGTEIVNAV	120
121	Qy	EVNRSNRNQEISGEYTI EAWTXFPDPGGRGNTHSNFKRWYHFDGTDWQSRQLQNKIKYF	180
121	Db	EVNRSNRNQETSGEYIAEAWTIFXFPDPGGRGNHSSFKRWYHFDGTDWQSRQLQNKIKYF	180
181	Qy	RGTGKAWDDEVDIENGNYDI LAYADIDMDHP EVINELRNMGVWYVNTLNLGDFRIDAVKH	240
181	Db	RGTGKAWDDEVDTEGNYDI LAYADVDDMDHP EVINELRNMGVWYVNTLNLGDFRIDAVKH	240
241	Qy	IKYSYTRDMLTHVRNRTGKPMFAVAFKFNKDLAA TENYLNKT SWNHSFVDPVPLHYNLNA	300
241	Db	IKYSYTRDMLTHVRNRTGKPMFAVAFKFNKDLGA IENYLNKT SWNHSFVDPVPLHYNLNA	300
301	Qy	SNSGGYFDMRNILNGSVQGHPIH AVTFVDNHDSPGGEALSFVQSWFKPLAYAILITRE	360
301	Db	SNSGGYFDMRNILNGSVQGHPIH AVTFVDNHDSPGGEALSFVQSWFKPLAYAILVLTRE	360
361	Qy	QGYPSVFYGDYIGIP THGVPSMKSKIDP LLLQARQIYAYGTQHDYFDHHDIIIGWTRBEGSS	420
361	Db	QGYPSVFYGDYIGIP THGVPSMKSKIDP LLLQARQIFAYGTQHDYFDHHDIIIGWTRBEGNS	420
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421	Db	HPNSGLATTMSDGP GGNKWMYVGGKNKAGQVWRDITGNRTCTVTINADGMGNFSVNGGSSV	480
481	Qy	VWVKQ 485	
481	Db	VWVKQ 485	

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RESULT 2
US-08-861-837-1
; Sequence 1, Application US/08861837
; Patent No. 5856164
; GENERAL INFORMATION:
; APPLICANT: Ottrup, Helle
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Ostergaard, Peter Rahbek
; APPLICANT: Rasmussen, Michael Dolberg
; APPLICANT: Van Der Zee, Pia
; TITLE OF INVENTION: Alkaline Bacillus Amylase
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESSES:
; ADDRESS: No. 5856164o No. 5856164disk of No. 5856164th America
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/861,837
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/446,803
; FILING DATE: 01-June-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Harrington, James J.
; REGISTRATION NUMBER: 38,711
; REFERENCE/DOCKET NUMBER: 4157.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 867-0123

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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/600,908A
; FILING DATE: 13-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Reza
; REGISTRATION NUMBER: 38,475
; REFERENCE/DOCKET NUMBER: 4394.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 485 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-600-908A-12

; ADDRESS: No. 60227240 No. 6022724disk of No. 6022724th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/683,838A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/600,908
; FILING DATE: 13-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Reza
; REGISTRATION NUMBER: 38,475
; REFERENCE/DOCKET NUMBER: 4394.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 485 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-683-838A-12

Query Match          96.3%; Score 2613; DB 2; Length 485;
Best Local Similarity 95.1%; Pred. No. 2.7e-223;
Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

QY 1 HHNGTGTMMQYFEWHLPLNDGNHNRLRDDAANKLSKGITAVWIPPAWKTSQNDVGGA 60
Db 1 HHNGTGTMMQYFEWHLPLNDGNHNRLRDDAANKLSKGITAVWIPPAWKTSQNDVGGA 60
QY 61 YDLYDLGEFNGKQTVRTKYGTRNQLQAATSLKNGGIQYGVVMMHKGADGTEIVNAV 120
Db 61 YDLYDLGEFNGKQTVRTKYGTRNQLQAATSLKNGGIQYGVVMMHKGADGTEIVNAV 120
QY 121 EVNRSNRNDEISGEYTIKTEAWTKFDFGCGNTHSNFKRWYHFDGTDQDQSRQLQNKIYKF 180
Db 121 EVNRSNRNDEISGEYTIKTEAWTKFDFGCGNTHSNFKRWYHFDGTDQDQSRQLQNKIYKF 180
QY 181 RGTGKAWDEVDIENGNDYLYMADIDMDHPEVINELRNMGVWYTNPLNDGFRIDAVKH 240
Db 181 RGTGKAWDEVDIENGNDYLYMADIDMDHPEVINELRNMGVWYTNPLNDGFRIDAVKH 240
QY 241 IKYSYTRDLWTHVRNTTGKPMFAVEFWKNDLAAIENYLNKTSWNHVSFVDPVPLHYNLYNA 300
Db 241 IKYSYTRDLWTHVRNTTGKPMFAVEFWKNDLAAIENYLNKTSWNHVSFVDPVPLHYNLYNA 300
QY 301 SNSSGYDFMRNILNGSVVQKHPHATVFDNDHDSQPCEALESFVQWFKPLAYALILTRE 360
Db 301 SNSSGYDFMRNILNGSVVQKHPHATVFDNDHDSQPCEALESFVQWFKPLAYALILTRE 360
QY 361 QGYPSVFGYDYGIPTHGVPSMKSIDPLQARQTYAGTQHDYFDHDDIIGWTREGDSS 420
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Db 421 HPNSGLATIMSDGPGGNKMYGKHAGQVWRDITGNRSCTVTINADGWNFTVNGGVS 480
QY 481 VVYKQ 485
Db 481 VVYKQ 485

RESULT 4
US-08-683-838A-12
; Sequence 12, Application US/08683838A
; Patent No. 6022724
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisg rd-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: Amylase Mutants
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
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5
RESULT
US-08-600-656-1
: Sequence 1, Application US/08600656
: Patent No. 6093562
: GENERAL INFORMATION:
: APPLICANT: Bisgard-Frantzen, Henrik
: APPLICANT: Svendsen, Allan
: APPLICANT: Borchert, Torben Vedel
: TITLE OF INVENTION: AMYLASE VARIANTS
: NUMBER OF SEQUENCES: 32
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: No. 6093562o No. 6093562disk of No. 6093562th America, Inc.
: STREET: 405 Lexington Avenue, Suite 6400
: CITY: New York
: STATE: New York
: COUNTRY: U.S.A.
: ZIP: 10174-6401
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
: CURRENT APPLICATION DATA: US/08/600.656
: APPLICATION NUMBER: US/08/600.656
: FILING DATE: 13-FEB-1996
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Lambiris, Elias J.
: REGISTRATION NUMBER: 33,728
: REFERENCE/DOCKET NUMBER: 4318.204-US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 212 867 0123
: TELEFAX: 212 867 0298
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 485 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
US-08-600-656-1

Query Match 96.3%; Score 2613; DB 3; Length 485;
Best Local Similarity 95.1%; Pred. No. 2.7e-223;
Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;
Qy 1 HNGTNGTMMQYFEWHLPLNDGNHWNRLRDDAANKSKGITAVWIPPAWKGTSONDVGGA 60
Db 1 HNGTNGTMMQYFEWHLPLNDGNHWNRLRDDAANKSKGITAVWIPPAWKGTSONDVGGA 60
Qy 61 YDLVDLGEFNKGKGVTRTKYGRSLOGAVTSLKKNNGIOVYGDVVMNHNKGGADGTEMVNAV 120
Db 61 YDLVDLGEFNKGKGVTRTKYGRNLOQAATSLKKNNGIOVYGDVVMNHNKGGADGTEMVNAV 120
Qy 121 EVNRSNRNOEISGEYTTIEAWTKFDPGGRNTHSNFKRWYHFDGTDWDSQRLQNKIYKF 180
Db 121 EVNRSNRNOETSGEYATIEAWTKFDPGGRNTHSNFKRWYHFDGTDWDSQRLQNKIYKF 180
Qy 181 RGTGKAWDEWDIENGNYDILMYADIMDHPEVINELRNWGVWYTNLNLGDFRIDAVKH 240
Db 181 RGTGKAWDEVDTEGNYDILMYADVDMHPEVIELRNWGVWYTNLNLGDFRIDAVKH 240
Qy 241 IKYSYTRDLWLTHTVNTTGKPMFAEAFWKNDLAAIENYLNKTSNNHSVDFVPLHNLNA 300
Db 241 IKYSYTRDLWLTHTVNTTGKPMFAEAFWKNDLGAIENYLNKTSNNHSVDFVPLHNLNA 300
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Db 301 SNSGGYFDMRNILGNSVQKHPHIAVTFVDNHDSDQPEALESFVQSWFKPLAYALILTRE 360
Qy 361 QYPSVFGDYGIPTTHGVPSMKSKIDPLQARQTYAGTQHDYFDHHDIIIGWTRREGSS 420
Db 361 QYPSVFGDYGIPTTHGVPSMKSKIDPLQARQTYAGTQHDYFDHHDIIIGWTRREGSS 420
Qy 421 HPNSGLATIMSDGPGGNKWMYVGNKAGQVWRDITGNRSQVTTINADGWGNTVNGGAVS 480
Db 421 HPNSGLATIMSDGPGGNKWMYVGNKAGQVWRDITGNRSQVTTINADGWGNTVNGGAVS 480

Qy 361 QYPSVFGDYGIPTTHGVPSMKSKIDPLQARQTYAGTQHDYFDHHDIIIGWTRREGSS 420
Db 361 QYPSVFGDYGIPTTHGVPSMKSKIDPLQARQTYAGTQHDYFDHHDIIIGWTRREGSS 420
Qy 421 HPNSGLATIMSDGPGGNKWMYVGNKAGQVWRDITGNRSQVTTINADGWGNTVNGGAVS 480
Db 421 HPNSGLATIMSDGPGGNKWMYVGNKAGQVWRDITGNRSQVTTINADGWGNTVNGGAVS 480
Qy 481 VWVKQ 485
Db 481 VWVKQ 485
RESULT 6
US-09-170-670-1
: Sequence 1, Application US/09170670
: Patent No. 6187576
: GENERAL INFORMATION:
: APPLICANT: Svendsen, Allan
: APPLICANT: Borchert, Torben
: APPLICANT: Bisgard-Frantzen Henrik
: TITLE OF INVENTION: Alpha-Amylase Mutants
: FILE REFERENCE: 5276.200-US
: CURRENT APPLICATION NUMBER: US/09/170.670
: CURRENT FILING DATE: 1998-10-13
: EARLIER APPLICATION NUMBER: 1172/97
: EARLIER FILING DATE: 1997-10-13
: EARLIER APPLICATION NUMBER: 60/063,306
: EARLIER FILING DATE: 1997-10-28
: NUMBER OF SEQ ID NOS: 22
: SOFTWARE: FastSEQ for Windows Version 3.0
: SEQ ID NO 1
: LENGTH: 485
: TYPE: PRT
: ORGANISM: Bacillus sp.
US-09-170-670-1

Query Match 96.3%; Score 2613; DB 4; Length 485;
Best Local Similarity 95.1%; Pred. No. 2.7e-223;
Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;
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Db 1 HNGTNGTMMQYFEWHLPLNDGNHWNRLRDDAANKSKGITAVWIPPAWKGTSONDVGGA 60
Qy 61 YDLVDLGEFNKGKGVTRTKYGRSLOGAVTSLKKNNGIOVYGDVVMNHNKGGADGTEMVNAV 120
Db 61 YDLVDLGEFNKGKGVTRTKYGRNLOQAATSLKKNNGIOVYGDVVMNHNKGGADGTEMVNAV 120
Qy 121 EVNRSNRNOEISGEYTTIEAWTKFDPGGRNTHSNFKRWYHFDGTDWDSQRLQNKIYKF 180
Db 121 EVNRSNRNOETSGEYATIEAWTKFDPGGRNTHSNFKRWYHFDGTDWDSQRLQNKIYKF 180
Qy 181 RGTGKAWDEWDIENGNYDILMYADIMDHPEVINELRNWGVWYTNLNLGDFRIDAVKH 240
Db 181 RGTGKAWDEVDTEGNYDILMYADVDMHPEVIELRNWGVWYTNLNLGDFRIDAVKH 240
Qy 241 IKYSYTRDLWLTHTVNTTGKPMFAEAFWKNDLAAIENYLNKTSNNHSVDFVPLHNLNA 300
Db 241 IKYSYTRDLWLTHTVNTTGKPMFAEAFWKNDLGAIENYLNKTSNNHSVDFVPLHNLNA 300
Qy 301 SNSGGYFDMRNILGNSVQKHPHIAVTFVDNHDSDQPEALESFVQSWFKPLAYALILTRE 360
Db 301 SNSGGYFDMRNILGNSVQKHPHIAVTFVDNHDSDQPEALESFVQSWFKPLAYALILTRE 360
Qy 361 QYPSVFGDYGIPTTHGVPSMKSKIDPLQARQTYAGTQHDYFDHHDIIIGWTRREGSS 420
Db 361 QYPSVFGDYGIPTTHGVPSMKSKIDPLQARQTYAGTQHDYFDHHDIIIGWTRREGSS 420
Qy 421 HPNSGLATIMSDGPGGNKWMYVGNKAGQVWRDITGNRSQVTTINADGWGNTVNGGAVS 480
Db 421 HPNSGLATIMSDGPGGNKWMYVGNKAGQVWRDITGNRSQVTTINADGWGNTVNGGAVS 480

QY 481 VVVKQ 485
 Db 481 VVVKQ 485

RESULT 7
 US-09-170-670-7
 ; Sequence 7, Application US/09170670
 ; Patent No. 6167576
 ; GENERAL INFORMATION:
 ; APPLICANT: Svendsen, Allan
 ; APPLICANT: Bisgaard-Frantzen, Henrik
 ; TITLE OF INVENTION: Alpha-Amylase Mutants
 ; FILE REFERENCE: 5276.200-US
 ; CURRENT APPLICATION NUMBER: US/09/170,670
 ; CURRENT FILING DATE: 1998-10-13
 ; EARLIER APPLICATION NUMBER: 1172/97
 ; EARLIER FILING DATE: 1997-10-13
 ; EARLIER APPLICATION NUMBER: 60/063,306
 ; NUMBER OF SEQ ID NOS: 22
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 7
 ; LENGTH: 485
 ; TYPE: PRT
 ; ORGANISM: Bacillus sp.
 US-09-170-670-7

Query Match 96.3%; Score 2613; DB 4; Length 485;
 Best Local Similarity 95.1%; Pred. No. 2.7e-223;
 Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

QY 1 HNGTNGTMMQYFEWHLPLNDGNHNRLRDAANLKSKITAVWIPPAWKGTSONDVGYGA 60
 Db 1 HNGTNGTMMQYFEWHLPLNDGNHNRLRDAANLKSKITAVWIPPAWKGTSONDVGYGA 60
 QY 61 YLDYDLGEFNGKQGTVRTKYGTSQLOQAVTSLKNNGIQVYGVVNMHKGADGTEVNAV 120
 Db 61 YLDYDLGEFNGKQGTVRTKYGTSQLOQAVTSLKNNGIQVYGVVNMHKGADGTEVNAV 120
 QY 121 EVNRSNRNOEISGEYTIKAWTKFDFPGRGNTHSNFKRWYHFDGTDWDSQRLQNKIYKF 180
 Db 121 EVNRSNRNOEISGEYTIKAWTKFDFPGRGNTHSNFKRWYHFDGTDWDSQRLQNKIYKF 180
 QY 181 RGTGKAWDEVDIENGNYDLYADIDMDHPEVINELRNWGVWYTNLNDGFRIDAVKH 240
 Db 181 RGTGKAWDEVDIENGNYDLYADIDMDHPEVINELRNWGVWYTNLNDGFRIDAVKH 240
 QY 241 IKYSYTRDLTHVRNTTGKPMFAVEFKNDLAAIENYLNKTSWNHVSFVDFVPLHYNLYNA 300
 Db 241 IKYSYTRDLTHVRNTTGKPMFAVEFKNDLAAIENYLNKTSWNHVSFVDFVPLHYNLYNA 300
 QY 301 SNSGGYDMRNILNGSVQKHPHATVTFVDNHDSPQGEALSFVQSWFKPLAYALVLTRE 360
 Db 301 SNSGGYDMRNILNGSVQKHPHATVTFVDNHDSPQGEALSFVQSWFKPLAYALVLTRE 360
 QY 361 QGYPSVFYGDYGIPTGHGVPMSKSIDPLQARQTYAGTQHDYFDHHDIIIGWTRREGDSS 420
 Db 361 QGYPSVFYGDYGIPTGHGVPMSKSIDPLQARQTYAGTQHDYFDHHDIIIGWTRREGDSS 420
 QY 421 HPNSGLATIMSDGPGGNKMWYVCKHKGAGQVWRDITNRSCTVTINADGNGFNFTVNGGVS 480
 Db 421 HPNSGLATIMSDGPGGNKMWYVCKHKGAGQVWRDITNRSCTVTINADGNGFNFTVNGGVS 480

QY 481 VVVKQ 485
 Db 481 VVVKQ 485

RESULT 8

US-09-193-068-1
 ; Sequence 1, Application US/09193068
 ; Patent No. 6197565
 ; GENERAL INFORMATION:
 ; APPLICANT: Svendsen, Allan
 ; APPLICANT: Kjrulff, S ren
 ; APPLICANT: Bisgaard-Frantzen, Henrik
 ; APPLICANT: Andersen, Carsten
 ; TITLE OF INVENTION: -Amylase Variants
 ; FILE REFERENCE: 5709.000-US
 ; CURRENT APPLICATION NUMBER: US/09/193,068
 ; CURRENT FILING DATE: 1998-11-16
 ; NUMBER OF SEQ ID NOS: 31
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 1
 ; LENGTH: 485
 ; TYPE: PRT
 ; ORGANISM: Bacillus sp.
 US-09-193-068-1

Query Match 96.3%; Score 2613; DB 4; Length 485;
 Best Local Similarity 95.1%; Pred. No. 2.7e-223;
 Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

QY 1 HNGTNGTMMQYFEWHLPLNDGNHNRLRDAANLKSKITAVWIPPAWKGTSONDVGYGA 60
 Db 1 HNGTNGTMMQYFEWHLPLNDGNHNRLRDAANLKSKITAVWIPPAWKGTSONDVGYGA 60
 QY 61 YLDYDLGEFNGKQGTVRTKYGTSQLOQAVTSLKNNGIQVYGVVNMHKGADGTEVNAV 120
 Db 61 YLDYDLGEFNGKQGTVRTKYGTSQLOQAVTSLKNNGIQVYGVVNMHKGADGTEVNAV 120
 QY 121 EVNRSNRNOEISGEYTIKAWTKFDFPGRGNTHSNFKRWYHFDGTDWDSQRLQNKIYKF 180
 Db 121 EVNRSNRNOEISGEYTIKAWTKFDFPGRGNTHSNFKRWYHFDGTDWDSQRLQNKIYKF 180
 QY 181 RGTGKAWDEVDIENGNYDLYADIDMDHPEVINELRNWGVWYTNLNDGFRIDAVKH 240
 Db 181 RGTGKAWDEVDIENGNYDLYADIDMDHPEVINELRNWGVWYTNLNDGFRIDAVKH 240
 QY 241 IKYSYTRDLTHVRNTTGKPMFAVEFKNDLAAIENYLNKTSWNHVSFVDFVPLHYNLYNA 300
 Db 241 IKYSYTRDLTHVRNTTGKPMFAVEFKNDLAAIENYLNKTSWNHVSFVDFVPLHYNLYNA 300
 QY 301 SNSGGYDMRNILNGSVQKHPHATVTFVDNHDSPQGEALSFVQSWFKPLAYALVLTRE 360
 Db 301 SNSGGYDMRNILNGSVQKHPHATVTFVDNHDSPQGEALSFVQSWFKPLAYALVLTRE 360
 QY 361 QGYPSVFYGDYGIPTGHGVPMSKSIDPLQARQTYAGTQHDYFDHHDIIIGWTRREGDSS 420
 Db 361 QGYPSVFYGDYGIPTGHGVPMSKSIDPLQARQTYAGTQHDYFDHHDIIIGWTRREGDSS 420
 QY 421 HPNSGLATIMSDGPGGNKMWYVCKHKGAGQVWRDITNRSCTVTINADGNGFNFTVNGGVS 480
 Db 421 HPNSGLATIMSDGPGGNKMWYVCKHKGAGQVWRDITNRSCTVTINADGNGFNFTVNGGVS 480
 QY 481 VVVKQ 485
 Db 481 VVVKQ 485

RESULT 9
 US-09-193-068-7
 ; Sequence 7, Application US/09193068
 ; Patent No. 6197565
 ; GENERAL INFORMATION:
 ; APPLICANT: Svendsen, Allan
 ; APPLICANT: Kjrulff, S ren
 ; APPLICANT: Bisgaard-Frantzen, Henrik
 ; APPLICANT: Andersen, Carsten
 ; TITLE OF INVENTION: -Amylase Variants
 ; FILE REFERENCE: 5709.000-US

; EARLIER APPLICATION NUMBER: PA 1998 00936
; EARLIER FILING DATE: 1998-07-14
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-183-412-7

Query Match 96.3%; Score 2613; DB 4; Length 485;
Best Local Similarity 95.1%; Pred. No. 2.7e-223;
Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

QY 1 HHNGTNGTMMQYFEWHLPLNDGNHNRLRDDAANKSGITAVWIPPAWKTSQNDVGCGA 60
DB 1 HHNGTNGTMMQYFEWHLPLNDGNHNRLRDDAANKSGITAVWIPPAWKTSQNDVGCGA 60
QY 61 YDLYDLGEFNQKGTVRTKYGTRSLQLOGAVTSLKNGGIQVYGVVNMHKGADGTEMYNAV 120
DB 61 YDLYDLGEFNQKGTVRTKYGTRSLQLOGAVTSLKNGGIQVYGVVNMHKGADGTEMYNAV 120
QY 121 EVNRSNRNQETISGEYTIKFTDFPCGRGNTSHNFKRWYHFDGTDQSRQLQNKIYKF 180
DB 121 EVNRSNRNQETISGEYTIKFTDFPCGRGNTSHNFKRWYHFDGTDQSRQLQNKIYKF 180
QY 181 RGTGKAWDEVDTENGNYDYLMTADMDHPEVINELRNMGVWYTNLTNDGFRIDAVKH 240
DB 181 RGTGKAWDEVDTENGNYDYLMTADMDHPEVINELRNMGVWYTNLTNDGFRIDAVKH 240
QY 241 IKYSYTRDMLTHVRNTTGGKPMFAVEFWKNDLAAIENYLNKTSWNHSHVDFVPLHYNLYNA 300
DB 241 IKYSYTRDMLTHVRNTTGGKPMFAVEFWKNDLAAIENYLNKTSWNHSHVDFVPLHYNLYNA 300
QY 301 SNSSGGYDMRNILNGSVVQKHPHATVFDVNDHDSQPCEALESFVQWFKPLAYALVLTRE 360
DB 301 SNSSGGYDMRNILNGSVVQKHPHATVFDVNDHDSQPCEALESFVQWFKPLAYALVLTRE 360
QY 361 QGYPSVFYGDYIGIPTHGVSPKMSKIDPLQARQTYAYGTHQHYFDHDIIGWTREGDSS 420
DB 361 QGYPSVFYGDYIGIPTHGVSPKMSKIDPLQARQTYAYGTHQHYFDHDIIGWTREGDSS 420
QY 421 HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTGTINADGWNFTVNGGVS 480
DB 421 HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTGTINADGWNFTVNGGVS 480
QY 481 VVWKQ 485
DB 481 VVWKQ 485

RESULT 12
US-09-354-191A-1
; Sequence 1, Application US/09354191A
; Patent No. 6297038
; GENERAL INFORMATION:
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: AMYLASE VARIANTS
; NUMBER OF SEQUENCE: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 62970380 No. 6297038disk of No. 6297038th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/354,191A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/600,656
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4318.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 867 0298
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 485 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-354-191A-1

Query Match 96.3%; Score 2613; DB 4; Length 485;
Best Local Similarity 95.1%; Pred. No. 2.7e-223;
Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

QY 1 HHNGTNGTMMQYFEWHLPLNDGNHNRLRDDAANKSGITAVWIPPAWKTSQNDVGCGA 60
DB 1 HHNGTNGTMMQYFEWHLPLNDGNHNRLRDDAANKSGITAVWIPPAWKTSQNDVGCGA 60
QY 61 YDLYDLGEFNQKGTVRTKYGTRSLQLOGAVTSLKNGGIQVYGVVNMHKGADGTEMYNAV 120
DB 61 YDLYDLGEFNQKGTVRTKYGTRSLQLOGAVTSLKNGGIQVYGVVNMHKGADGTEMYNAV 120
QY 121 EVNRSNRNQETISGEYTIKFTDFPCGRGNTSHNFKRWYHFDGTDQSRQLQNKIYKF 180
DB 121 EVNRSNRNQETISGEYTIKFTDFPCGRGNTSHNFKRWYHFDGTDQSRQLQNKIYKF 180
QY 181 RGTGKAWDEVDTENGNYDYLMTADMDHPEVINELRNMGVWYTNLTNDGFRIDAVKH 240
DB 181 RGTGKAWDEVDTENGNYDYLMTADMDHPEVINELRNMGVWYTNLTNDGFRIDAVKH 240
QY 241 IKYSYTRDMLTHVRNTTGGKPMFAVEFWKNDLAAIENYLNKTSWNHSHVDFVPLHYNLYNA 300
DB 241 IKYSYTRDMLTHVRNTTGGKPMFAVEFWKNDLAAIENYLNKTSWNHSHVDFVPLHYNLYNA 300
QY 301 SNSSGGYDMRNILNGSVVQKHPHATVFDVNDHDSQPCEALESFVQWFKPLAYALVLTRE 360
DB 301 SNSSGGYDMRNILNGSVVQKHPHATVFDVNDHDSQPCEALESFVQWFKPLAYALVLTRE 360
QY 361 QGYPSVFYGDYIGIPTHGVSPKMSKIDPLQARQTYAYGTHQHYFDHDIIGWTREGDSS 420
DB 361 QGYPSVFYGDYIGIPTHGVSPKMSKIDPLQARQTYAYGTHQHYFDHDIIGWTREGDSS 420
QY 421 HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTGTINADGWNFTVNGGVS 480
DB 421 HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTGTINADGWNFTVNGGVS 480
QY 481 VVWKQ 485
DB 481 VVWKQ 485

RESULT 13
US-09-264-097-7
; Sequence 7, Application US/09264097
; Patent No. 6287826
; GENERAL INFORMATION:
; APPLICANT: No. 6287826man, Barrie Edmund
; APPLICANT: Hendriksen, Hanne Vang

```

RESULT 14
US-08-446-803-2
; Sequence 2, Application US/08446803
; Patent No. 5824531
; GENERAL INFORMATION:
; APPLICANT: Ottrup, Helle
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Ostergaard, Peter, Rahbek
; APPLICANT: Rasmussen, Michael Dolberg
; APPLICANT: Van Der Zee, Pia
; TITLE OF INVENTION: Alkaline Amylase
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5824531o No. 5824531disk of No. 5824531th America

```

US-08-861-837-2
; Sequence 2, Application US/08861837
; Patent No. 5856164
; GENERAL INFORMATION:
; APPLICANT: Ottrup, Helle
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Ostergaard, Peter Rahbek
; APPLICANT: Rasmussen, Michael Dolberg
; APPLICANT: Van Der Zee, Pia
; TITLE OF INVENTION: Alkaline Bacillus Amylase
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5856164o No. 5856164disk of No. 5856164th America
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/861,837
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/446,803
; FILING DATE: 01-June-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Harrington, James J.
; REGISTRATION NUMBER: 38,711
; REFERENCE/DOCKET NUMBER: 4157.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 867-0123
; TELEFAX: (212) 878-9655
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 485 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-861-837-2

Query Match 89.9%; Score 2440; DB 2; Length 485;
Best Local Similarity 86.6%; Pred. No. 5.6e-208;
Matches 420; Conservative 40; Mismatches 25; Indels 0; Gaps 0;

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QY	61	YDLYDLGEFNKGTGRTKYGTSQLQGAVALSKNNGIQVYGDVVMNHKGGADGTEMYNAV	120
DB	61	YDLYDLGEFNKGTGRTKYGTSQLQGAVALSKNNGIQVYGDVVMNHKGGADATENVLAV	120
QY	121	EVNRSNRNQEISGEYTTIATWTKFDGPGRGNTSHNFKRWYHFDGTDWDSRQLQNKIYKF	180
DB	121	EVAPNNRNQEISGDYTTIATWTKFDGPGRGNTSDFKRWYHFDGVDWDSRQFQNRIFYE	180
QY	181	RGTKKAWDEVDIENGNYDYLWADIDMDHPEVINELRNNGVWYTNLTNLDGFRIDAVKH	240
DB	181	RGDGKAWDEVDSENGNYDYLWADIDMDHPEVINELRNNGVWYTNLTNLDGFRIDAVKH	240
QY	241	IKYSYTRDLWLTHTVNTTCKPMFAVAEFKNDLAAIENYLNKTSNHSVFDVPLHLYNA	300
DB	241	IKYSYTRDLWLTHTVNTTCKPMFAVAEFKNDLGALENYLNKTSNHSVFDVPLHLYNA	300
QY	301	SNSGGYEDMRNILNGSVVQKHPHVAFTVDNHDSPQGESLESFVQWFKPLAYALILTRE	360

Db	301	SNSGGYDMAKLLNGTVVQKHPHVAFTVDNHDSPQGESLESFVQWFKPLAYALILTRE	360
QY	361	QGYPSVFYGDYVGIPTTHGVPSMSKIDPLLAQARTYAVGTQHDYFDHDDIIGWTREGDSS	420
Db	361	QGYPSVFYGDYVGIPTTHGVPSMSKIDPLLAQARTYAVGTQHDYFDHDDIIGWTREGDSS	420
QY	421	HPNSGLATIMSDGPGGNKWMYVGVKHKAGQVWRDITGNRSGETVTINADGWNFTVNGGAVS	480
Db	421	HPNSGLATIMSDGPGGKWMYVGVKHKAGQVWHDITGNKPGTGTINADGWNFTVNGGAVS	480
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Db	481	IWVKR	485

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 28, 2001, 16:58:04 ; Search time 33.83 Seconds
(without alignments)
1061.943 Million cell updates/sec

Title: US-09-590-375-2

Perfect score: 2713

Sequence: 1 HHNGTNGTMQYFEWHLFND.....ADGWGNETVNGAVVWVKQ 485

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: /SIDS2/gcgdata/geneseq/geneseq/AA1982.DAT.*
4: /SIDS2/gcgdata/geneseq/geneseq/AA1983.DAT.*
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22: /SIDS2/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2713	100.0	516	18 AAW11326	Alkaline liquefyin
2	2704	99.7	485	19 AAW79904	Liquefied alkaline
3	2700	99.5	516	21 AAB35714	Mutant alpha-amylase
4	2613	96.3	485	18 AAW31499	Bacillus sp. alpha
5	2613	96.3	485	19 AAW48260	Bacillus sp. alpha
6	2613	96.3	485	20 AAY25150	Bacillus sp. alpha
7	2613	96.3	485	20 AAY15415	Bacillus strain NC
8	2613	96.3	485	20 AAY15421	Teramyl-like alpha
9	2613	96.3	485	20 AAY07381	Wild type Teramyl
10	2613	96.3	485	20 AAY07391	Wild type Teramyl
11	2613	96.3	485	21 AAY99602	Bacillus parent Te

12	2613	96.3	485	21	AA999608	Bacillus Teramyl-
13	2611	96.2	485	17	AAW12113	Alpha-amylase vari
14	2610	96.2	485	17	AAW12129	Alpha-amylase vari
15	2610	96.2	485	17	AAW12130	Alpha-amylase vari
16	2610	96.2	485	17	AAW12119	Alpha-amylase vari
17	2610	96.2	485	17	AAW12120	Alpha-amylase vari
18	2610	96.2	485	17	AAW12121	Alpha-amylase vari
19	2610	96.2	485	17	AAW12118	Alpha-amylase vari
20	2610	96.2	485	17	AAW12102	Alpha-amylase vari
21	2610	96.2	485	17	AAW12103	Alpha-amylase vari
22	2610	96.2	485	17	AAW12104	Alpha-amylase vari
23	2610	96.2	485	17	AAW12105	Alpha-amylase vari
24	2610	96.2	485	17	AAW12106	Alpha-amylase vari
25	2610	96.2	485	17	AAW12107	Alpha-amylase vari
26	2610	96.2	485	17	AAW12108	Alpha-amylase vari
27	2610	96.2	485	17	AAW12098	Alpha-amylase vari
28	2610	96.2	485	17	AAW12099	Alpha-amylase vari
29	2610	96.2	485	17	AAW12100	Alpha-amylase vari
30	2609	96.2	485	17	AAW12114	Alpha-amylase vari
31	2609	96.2	485	17	AAW12117	Alpha-amylase vari
32	2608	96.1	485	17	AAW12127	Alpha-amylase vari
33	2608	96.1	485	17	AAW12128	Alpha-amylase vari
34	2608	96.1	485	17	AAW12131	Alpha-amylase vari
35	2608	96.1	485	17	AAW12122	Alpha-amylase vari
36	2608	96.1	485	17	AAW12123	Alpha-amylase vari
37	2608	96.1	485	17	AAW12124	Alpha-amylase vari
38	2608	96.1	485	17	AAW12125	Alpha-amylase vari
39	2608	96.1	485	17	AAW12126	Alpha-amylase vari
40	2607	96.1	485	17	AAW12111	Alpha-amylase vari
41	2607	96.1	485	17	AAW12112	Alpha-amylase vari
42	2607	96.1	485	17	AAW12101	Alpha-amylase vari
43	2606	96.1	485	17	AAW12144	Alpha-amylase vari
44	2606	96.1	485	17	AAW12110	Alpha-amylase vari
45	2605	96.0	485	17	AAW12109	Alpha-amylase vari

ALIGNMENTS

RESULT 1
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ID AAW11326 standard; Protein; 516 AA.
XX
AC AAW11326;
XX
XX 11-NOV-1997 (first entry)
DT
XX
DE Alkaline liquefying alpha-amylase.
XX
KW Alkaline liquefying alpha-amylase; Bacillus; alpha-amylase; detergent;
KW starch-related polysaccharide; hydrolysis; enzyme; surfactant resistance;
KW alpha-1,4-glucosidic link; alkalophilic Bacillus; laundry detergent;
KW dish-washing detergent; starch.
XX
OS Bacillus species KSM-API378.
XX
PN WO9700324-A1.
XX
PD 03-JAN-1997.
XX
PF 14-JUN-1996; 96WO-JP01641.
XX
XX 14-JUN-1995; 95JP-0147257.
PR
XX (KAOS) KAO CORP.
PA
XX
XX
PI Ara K, Hatada Y, Ito S, Kawai S, Ozaki K.
DR WPI: 1997-118708/11.
DR N-PSDB; AAT51339.
XX
PT DNA encoding alkaline liquefying alpha-amylase - useful in
PT dish-washing and laundry detergents for removal of starch dirt

XX Claim 2; Page 23-26; 40pp; English.
 CC This sequence represents an alkaline liquefying alpha-amylase.
 CC Alpha-amylase is an enzyme that acts on starch-related polysaccharides,
 CC hydrolysing the alpha-1,4-glucoside bond of the polysaccharide molecule.
 CC Alkaline liquefying alpha-amylases exhibit resistance to surfactants used
 CC in detergents, and decompose starch or starch-related polysaccharides in
 CC a highly random manner. The Bacillus species KSM-Ap1378, from which this
 CC sequence was isolated, is an alkalophilic Bacillus strain. It was
 CC isolated from soil in the vicinity of the city of Tochi. The enzyme is
 CC useful in improving the efficiency of dish-washing and laundry
 CC detergents, particularly on starch dirt.
 XX SQ Sequence 516 AA;

Query Match 100.0%; Score 2713; DB 18; Length 516;
 Best Local Similarity 100.0%; Pred. No. 4.2e-219;
 Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HNGTNGTMMQYFEWHLDPNDGNHNRDRDAANLKSKGITAVWIPPAWKTSQNDVGGA 60
 DB 32 hngtngtmmqyfehwlpndgnhnrldrdaanlkskgitavwippawkgtsqndvggga 91
 QY 61 YDLYDLGFEFNOKGTVRTKYGRSLOQAVTSLKNNGIQVYGDVVMNHKGGADGTEMNAV 120
 DB 92 ydlydlgefnokgtvrtkygrslqgavtslknnqiqvgdvvmnhkggadgtemnav 151
 QY 121 EVNRSNRNOEISGEYITAEAWTKFDPGGRNTHSNFKWYHFDGTDWDSQRLQNKIYKF 180
 DB 152 evnrsnrngelsgeytleawtkfdpgrgnthsnfkwrwyhfdgtdwdsqrlqnkikyf 211
 QY 181 RGTCKANDWEVDIENGNYDLYMADIDMDHPEVINELRNMGVWYTNLNLGFRIDAVKH 240
 DB 212 rgtckandwevdiengnydlymadidmdhpevineelrnmgvwytnlnlgfridavkh 271
 QY 241 IKYSTTRDLWTHVRNTGKPMFAVAEFKNDLAAIENYLNKTSNNHVSFVDPPLHYNLYNA 300
 DB 272 ikysytrdlwthrntgkpmfavaefkndlaaienylktswnhsvfdvplhynlyna 331
 QY 301 SNSGGYFDMRNLGSSVQKHPHIAVTFVDNHDSPQGEALSFVQSFKPLAYALILTRE 360
 DB 332 snsnggyfdmrnlngssvqkhpiahvtfvndhdsqpgealesfvqsfkplayaliltre 391
 QY 361 QGYPSVFGYDYGIPTHGVPNSKIDPLLOARTYAYGTQHDYFDHHDITGWTREGDSS 420
 DB 392 qgypsvfygydypthgvpmskidlpllgartqaygtqhdvfdhhdiiigtregdss 451
 QY 421 HPNSGLATIMSDGPGGNKMWYGVKHKAGOVWRDITGNRSCTVTINADGWNFTYNGGAVS 480
 DB 452 hpnsglatimsdgp9gnkwmvvgkhagqvwrtditgnrsgtvtinadgwnftnggavs 511
 QY 481 VWVKQ 485
 DB 512 vwvkq 516

RESULT 2
 AA779904
 ID AA779904 standard; protein; 485 AA.
 XX
 AC AA779904;
 XX
 DT 18-DEC-1998 (first entry)
 XX
 DE Liquefied alkaline alpha-amylase.
 XX
 KW Liquefied alkaline alpha-amylase; mutation; Bacillus licheniformis;
 KW detergent; bleaching agent; oxidising agent.
 XX
 OS Bacillus licheniformis.
 XX

PH Key Location/Qualifiers
 FT Misc-difference 202
 FT /note= "can be deleted or substituted by another amino
 FT acid residue such as Thr, Ile, Leu, Ala, Val
 FT or Ser"
 XX WO9844126-A1.
 XX 08-OCT-1998.
 XX 31-MAR-1998; 98WO-JP01464.
 XX 31-MAR-1997; 97JP-0080299.
 XX (KAOS) KAO CORP.
 XX Hatada Y, Ikawa K, Ito S;
 XX WPI: 1998-542707/46.
 XX Bacillus derived alpha amylase having mutation at position 202
 PT has optimum pH in alkaline conditions and high tolerance to
 PT oxidants, useful for production of detergent compositions
 XX Claim 1; Page 19-21; 42pp; Japanese.
 XX The present sequence represents Bacillus licheniformis liquefied alkaline
 CC alpha-amylase. The present invention describes mutated forms of the
 CC liquefied alkaline alpha-amylase derived from Bacillus species KSM-Ap1378
 CC (FERM BP-3048), having the methionine residue at position 202 either
 CC deleted or substituted by another amino acid, such as threonine,
 CC isoleucine, leucine, alanine, valine or serine. The mutated enzyme may
 CC have other mutations (such as deletion of arginine or glycine at
 CC positions 181 and 182, respectively) but at least 95.2% homologous to
 CC the original enzyme. The mutated enzyme has optimum pH in alkaline
 CC conditions, a high alpha amylase activity, and a high and sustained
 CC tolerance to oxidising substances. The enzyme may be used in the
 CC formulation of liquid, powder or granular detergent compositions,
 CC especially those containing bleaches and oxidants. The enzyme retains
 CC high activity in the presence of bleaches and oxidants allowing improved
 CC detergent formulations to be produced.
 XX Sequence 485 AA;

Query Match 99.7%; Score 2704; DB 19; Length 485;
 Best Local Similarity 99.8%; Pred. No. 2.2e-218;
 Matches 484; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 HNGTNGTMMQYFEWHLDPNDGNHNRDRDAANLKSKGITAVWIPPAWKTSQNDVGGA 60
 DB 1 hngtngtmmqtfewhlpndgnhnrldrdaanlkskgitavwippawkgtsqndvggga 60
 QY 61 YDLYDLGFEFNOKGTVRTKYGRSLOQAVTSLKNNGIQVYGDVVMNHKGGADGTEMNAV 120
 DB 61 ydlydlgefnokgtvrtkygrslqgavtslknnqiqvgdvvmnhkggadgtemnav 120
 QY 121 EVNRSNRNOEISGEYITAEAWTKFDPGGRNTHSNFKWYHFDGTDWDSQRLQNKIYKF 180
 DB 121 evnrsnrngelsgeytleawtkfdpgrgnthsnfkwrwyhfdgtdwdsqrlqnkikyf 180
 QY 181 RGTCKANDWEVDIENGNYDLYMADIDMDHPEVINELRNMGVWYTNLNLGFRIDAVKH 240
 DB 181 rgtckandwevdiengnydlymadidmdhpevineelrnmgvwytnlnldgfridavkh 240
 QY 241 IKYSTTRDLWTHVRNTGKPMFAVAEFKNDLAAIENYLNKTSNNHVSFVDPPLHYNLYNA 300
 DB 241 ikysytrdlwthrntgkpmfavaefkndlaaienylktswnhsvfdvplhynlyna 300
 QY 301 SNSGGYFDMRNLGSSVQKHPHIAVTFVDNHDSPQGEALSFVQSFKPLAYALILTRE 360
 DB 301 snsnggyfdmrnlngssvqkhpiahvtfvndhdsqpgealesfvqsfkplayaliltre 360

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QY 361 QGYPVSFYGDYIGIPTHGVPSMKSIDPILLQARQTVAYGTQHDYFDHHDIIIGWTRGDSS 420
|||||
Db 361 qgypsvfygdyigipthgvpsmksidp||lqarqtaygtqhdyfhdhdiigwtrgdss 420
QY 421 HPNSGLATIMSDGPGGNKMYVCKHKAGQVWRDITGNRSCTVTINADGWCNFTVNGGAVS 480
|||||
Db 421 hpnsglatimsdpgpgnkmvvgkhkagqvwrdditnrgstvtinadgwgntfnggavs 480
QY 481 VVVKQ 485
|||||
Db 481 vvvkq 485

RESULT 3
AA35714
ID AAB35714 standard; protein; 516 AA.
XX
AC AAB35714;
XX
DT 19-FEB-2001 (first entry)
XX
DE Mutant alpha-amylase amino acid sequence.
XX
KW Alpha-amylase; detergent; Bacillus.
XX
OS Bacillus sp.
XX
FH Key
FT Misc-difference 297
FT /note= "Represented as Alu in the specification"
FT Misc-difference 335
FT /note= "Represented as Aly in the specification"
XX
PN JP2000245466-A.
XX
PD 12-SEP-2000.
XX
PF 25-FEB-1999; 99JP-0048213.
XX
PR 25-FEB-1999; 99JP-0048213.
XX
PA (KAOS ) KAO CORP.
XX
DR WPI; 2000-615143/59.
XX
DR N-PSDB; AAC66234.
XX
PT A novel mutant alpha-amylase for use in a detergent composition -
XX
PS Claim 1; Page 5-6; 12pp; Japanese.
XX
CC The present invention relates to a mutant alpha-amylase. Included in the
CC invention are a gene encoding the mutant alpha-amylase, a vector
CC containing the gene, and a transformed cell recombined by the vector. The
CC enzyme is used in a detergent composition. The present sequence
CC represents the mutant alpha-amylase protein.
XX
SQ Sequence 516 AA;

Query Match 99.5%; Score 2700; DB 21; Length 516;
Best Local Similarity 99.6%; Pred. No. 5.2e-218;
Matches 483; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 HNGTNGTMMQYFEWHLNDGNHNRRLRDAANLKSIGITAVWIPAWKGTSONDVGGA 60
|||||
Db 32 hngtntgmqyfewhlnpdngnhnrlddaanlksigitaavwippawkgtsqndvgga 91
|||||
QY 61 YDLYDLGEFNQKGTVRTKYGTSRQLQAGAVTSLKNNGIQYGVVMMNHKGADGTEMNAV 120
|||||
Db 92 ydlydlgefngkgtvrtkgytsrqlgavtslknngiqygvvmmnhkggagdgtemnav 151
|||||
QY 121 EVNRSNRNQEISGEYTEAWTKFDFGCRGNTSHSNFKRWYHFDGTQDQSRQLQNKIYKF 180
|||||
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Db 152 evnrsnrnqeisgeyteawtkfdfpgrgntshsnfkwrwyhfdgtdwdqsrqlqnkiykf 211
QY 181 RGTGKAWDEVDITENGNDYDLYMADIDMDHPEVINELRNHGVWYTTNLTNDGPRIDAVKH 240
|||||
Db 212 rgtgkaweveditengndydlmyadidmdhpevinelrnwgvwyttntclnldgfridavkh 271
|||||
QY 241 IKYSYTRDMLTHVRNTTGKPMFAVAEFWKNDLAAIENYLNKTSWNHSHVFDVPLHYNLYNA 300
|||||
Db 272 ikysytrdwlthvtrnttgkpmfavafxkndlaaienylnktswnhshvfdvplhynlyna 331
|||||
QY 301 SNSGGYFDMRNILNGSVVQKHPHIAVTFVDNHDSDQGEALESFVQSKPLAYALILTRE 360
|||||
Db 332 snsggyfdmrnilngsvvqkhpiahvtfvdnhdsgpgealesfvqskplayaliltre 391
|||||
QY 361 QGYPVSFYGDYIGIPTHGVPSMKSIDPILLQARQTVAYGTQHDYFDHHDIIIGWTRGDSS 420
|||||
Db 392 qgypsvfygdyigipthgvpsmksidp||lqarqtaygtqhdyfhdhdiigwtrgdss 451
|||||
QY 421 HPNSGLATIMSDGPGGNKMYVCKHKAGQVWRDITGNRSCTVTINADGWCNFTVNGGAVS 480
|||||
Db 452 hpnsglatimsdpgpgnkmvvgkhkagqvwrdditnrgstvtinadgwgntfnggavs 511
QY 481 VVVKQ 485
|||||
Db 512 vvvkq 516

RESULT 4
AA331499
ID AAW31499 standard; protein; 485 AA.
XX
AC AAW31499;
XX
DT 08-APR-1998 (first entry)
XX
DE Bacillus sp. alpha amylase.
XX
KW Alpha -amylase; hard surface cleaning; dishwashing; laundry.
XX
OS Bacillus sp.
XX
PN W09732961-A2.
XX
PD 12-SEP-1997.
XX
PF 04-MAR-1997; 97WO-US03635.
XX
PR 07-MAR-1996; 96WO-US03276.
XX
PA (PROC ) PROCTER & GAMBLE CO.
XX
PI Baeck AC, Jones LA, Ohtani R, Pramod K, Rai S;
PI Showell MS, Ward G;
XX
DR WPI; 1997-457524/42.
XX
PT Detergent compositions for hard surface cleaning and laundry use -
PT contains Bacillus derived alpha amylase with improved
PT thermostability, reduced calcium ion dependency etc.
XX
PS Claim 1; Pages 86-87; 97pp; English.
XX
CC The present sequence is a Bacillus sp. alpha amylase with a
CC specific activity at least 25% higher than that of Termamyl (RTM)
CC at 25 to 55 degrees C at pH 8 to 10, measured by the Phadebas (RTM)
CC activity test. It is of use in hard surface cleaning, hand or
CC machine dishwashing and laundry at a temperature of 10 to 25
CC degrees C. Improved cleaning, stain removal and fabric care
CC obtained by using it at a concentration of 0.00018 to 0.06%
XX
SQ Sequence 485 AA;
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Query Match 96.3%; Score 2613; DB 18; Length 485;
Best Local Similarity 95.1%; Pred. No. 9.3e-211;
Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

QY 1 HHNGTNGTMMQYFEWHLPNDGNHNRLRDDAANKSGKITAVWIPPAWKGSQNDVGGA 60
DB 1 hhgntngtmmqyfewyfpndgnhwnrlrddaanlkskgitavwippawkgsgndvgga 60

QY 61 YDLXDLGFEFNQKGVTRTKYKTRSQLOGAVTSLKNGGIQVYGDVVMNHKGGADGTEMNAV 120
DB 61 ydldxdlgfefnqkgtvrtkyktrsqlogavtslknggiqvdygdyvmnhkggadgteimnav 120

QY 121 EVNRSNRNQEISGEYTTAEATKFDPPGRGNTHSNPKRWYHFDGTDWDQSQLOLQNKIYKF 180
DB 121 evnrsnrnqetsgeyaieawtkfdppgrgnthsnpkwnhssfkwrwyhfdgtwdqsrqlqnkikyf 180

QY 181 RGTGKAWDEWDIENGNYDYLMDADIDMDHPEVINELRNWGVWYTNLTNLDGFRIDAVKH 240
DB 181 rgtgkawdewdtenydylymdadvmdhpevinelnwgvwytnltnldgfridavkh 240

QY 241 IKYSYTRDMLTHVRNTTGKPMFAVAEFKNDLAAIENYLNKTSWNHVSFVPLHYNLYNA 300
DB 241 ikysftrdmlthvtrnttgkpmfavaefwkndlgaienylnktswnhsvfplhynlyna 300

QY 301 SNSGGYFDMRNILNGSVVQKHPIHATVFDVNDHDSQGEALSFVQSKPLAYALILTRE 360
DB 301 snsggyydmrnilngsvvqkhphatvfdvndhdsqgealesfvqskplayaliltre 360

QY 361 QGYPSVFYGDYIGIPTHGVPMSKIDPLQAROTYAGTQHDYFDHDDIIGWTRREGDSS 420
DB 361 qgypsvfgydyigipthgvpamkskidplqarctfaygtqhdvfdhddiigwtrreguss 420

QY 421 HPNSGLATIMSDGPGGNKMWYGVKHKAGQVWRDITGNRSQVTITNADGWNFTVNGGAVS 480
DB 421 hpnsglatimsdpggnkwmvygknkagvwrtditgnrtgtvtinadgwnfsvnggsvs 480

QY 481 VWVKQ 485
DB 481 vvvkq 485

RESULT 5
AAW48260
ID AAW48260 standard; protein; 485 AA.
XX AC AAW48260;
XX DT 02-JUL-1998 (first entry)
XX DE Bacillus sp. alpha amylase protein #1.
XX Alpha amylase; stain digestion; detergent; fabric laundry performance.
XX KW Bacillus sp.
XX OS W09805748-A1.
XX PN 12-FEB-1998.
XX PD 01-AUG-1996; 96WO-US12612.
XX PF 01-AUG-1996; 96WO-US12612.
XX PR (PROC) PROCTER & GAMBLE CO.
XX PA Baeck AC, Jones LA, Ohtani R, Pramod K, Rai S;
XX PI Showell MS;
XX PT WPI; 1998-159168/14.
XX Use of specific alpha-amylase enzymes - in laundry detergent
PT compositions to provide effective cleaning and whitening of dingy
PT fabrics

XX Claim 1; Page 69-70; 82pp; English.
XX This sequence represents an alpha amylase from Bacillus sp. which is
CC used in a laundry detergent. The detergent compositions can be used
CC for boosting fabric laundry performance or for dingy
CC fabric cleanup.
XX SQ Sequence 485 AA;

Query Match 96.3%; Score 2613; DB 19; Length 485;
Best Local Similarity 95.1%; Pred. No. 9.3e-211;
Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

QY 1 HHNGTNGTMMQYFEWHLPNDGNHNRLRDDAANKSGKITAVWIPPAWKGSQNDVGGA 60
DB 1 hhgntngtmmqyfewyfpndgnhwnrlrddaanlkskgitavwippawkgsgndvgga 60

QY 61 YDLXDLGFEFNQKGVTRTKYKTRSQLOGAVTSLKNGGIQVYGDVVMNHKGGADGTEMNAV 120
DB 61 ydldxdlgfefnqkgtvrtkyktrsqlogavtslknggiqvdygdyvmnhkggadgteimnav 120

QY 121 EVNRSNRNQEISGEYTTAEATKFDPPGRGNTHSNPKRWYHFDGTDWDQSQLOLQNKIYKF 180
DB 121 evnrsnrnqetsgeyaieawtkfdppgrgnthsnpkwnhssfkwrwyhfdgtwdqsrqlqnkikyf 180

QY 181 RGTGKAWDEWDIENGNYDYLMDADIDMDHPEVINELRNWGVWYTNLTNLDGFRIDAVKH 240
DB 181 rgtgkawdewdtenydylymdadvmdhpevinelnwgvwytnltnldgfridavkh 240

QY 241 IKYSYTRDMLTHVRNTTGKPMFAVAEFKNDLAAIENYLNKTSWNHVSFVPLHYNLYNA 300
DB 241 ikysftrdmlthvtrnttgkpmfavaefwkndlgaienylnktswnhsvfplhynlyna 300

QY 301 SNSGGYFDMRNILNGSVVQKHPIHATVFDVNDHDSQGEALSFVQSKPLAYALILTRE 360
DB 301 snsggyydmrnilngsvvqkhphatvfdvndhdsqgealesfvqskplayaliltre 360

QY 361 QGYPSVFYGDYIGIPTHGVPMSKIDPLQAROTYAGTQHDYFDHDDIIGWTRREGDSS 420
DB 361 qgypsvfgydyigipthgvpamkskidplqarctfaygtqhdvfdhddiigwtrreguss 420

QY 421 HPNSGLATIMSDGPGGNKMWYGVKHKAGQVWRDITGNRSQVTITNADGWNFTVNGGAVS 480
DB 421 hpnsglatimsdpggnkwmvygknkagvwrtditgnrtgtvtinadgwnfsvnggsvs 480

QY 481 VWVKQ 485
DB 481 vvvkq 485

RESULT 6
AAW25150
ID AAW25150 standard; protein; 485 AA.
XX AC AAW25150;
XX DT 27-AUG-1999 (first entry)
XX DE Bacillus sp. alpha-amylase protein fragment 1.
XX Alpha-amylase; cleaning composition; protease variant; spot removal;
KW detergent composition; hard surface cleaning; fabric cleaning;
KW dishwashing composition; oral cleaning composition; personal cleansing;
KW stain removal; soil removal; whiteness maintenance; dingy cleanup;
KW film removal.
XX OS Bacillus sp.
XX PN W09920723-A2.
XX PT 29-APR-1999.

XX PF 23-OCT-1998; 98WO-US22486.
 XX PR 23-OCT-1997; 97US-0956564.
 XX PR 23-OCT-1997; 97US-0956323.
 XX PR 23-OCT-1997; 97US-0956324.
 XX PA (PROC) PROCTER & GAMBLE CO.
 XX PI Baek AC, Busch A, Ghosh CK, Ohtani R, Showell MS;
 XX DR WPI; 1999-404706/34.
 XX PT New cleaning compositions
 XX PS Claim 1b(ii); Page 164-165; 169pp; English.
 XX CC This invention describes novel cleaning compositions which contain a
 CC protease variant with an amino acid substitution corresponding to
 CC position 103 of Bacillus amyloliquefaciens and an alpha-amylase variant.
 CC The compositions can be used in e.g. detergent compositions, for cleaning
 CC hard surfaces or fabrics, dishwashing compositions, oral cleaning
 CC compositions, detergent cleaning compositions and personal cleansing
 CC compositions. The combination of protease variants and alpha-amylase
 CC variants in cleaning compositions can provide improved and enhanced
 CC cleaning ability, including stain and/or soil removal and/or reduction
 CC and/or whiteness maintenance and/or dingy cleanup and/or spot and/or
 CC film removal and/or reduction, over conventional enzyme-containing
 CC cleaning compositions.
 XX Sequence 485 AA;

Query Match 96.3%; Score 2613; DB 20; Length 485;
 Best Local Similarity 95.1%; Pred. No. 9.3e-211;
 Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

QY 1 HNGTNGTMMQYFEWHLPNDSGNHNRRLDDAANLKSIGITAVWIPPAWKTSONDYGCGA 60
 DB 1 hngtngtmmqyfewlylpndgnhnrlddaaanksgitavwippawkgtsqndvggga 60

QY 61 YDLYDLGEFNQKGTVRTKYGTSRQLOGAVTSLKNNGIQVYGVDMNHKGGADGTEWNAV 120
 DB 61 yldylgefnqgtvrtkygtrnqlqaavtslknngiqvgdvmmhkggadgteivnav 120

QY 121 EVNRSNRNOEISGEYTIKAWTKFDFPGRGNTHSNFKRWYHFDGTQDQSRQONKIYKF 180
 DB 121 evnrsnrnqetsgeyaaleawtkfdfpgrgnhssfkwyhfdgtwdgsrqlqnkiyxf 180

QY 181 RGTGKAWDEVDIENGNDYLYMADIDMDHPEVINELRNWGVWYTNLNLDFRIDAVKH 240
 DB 181 rgtgkawdevdtengndylymadvdmhpevihelrnwgvwytnlnldgfridavkh 240

QY 241 IKYSYTRDLTHVRNTGKPMFAVAFKNDLAAIENYLNKTSWNHSDVDFVPLHYLYNA 300
 DB 241 ikysftrdlthvrntgkpmfavaefwkndlgaliennylnktswnhsvdfvplhylyna 300

QY 301 SNSGGYFDMRNILNGSVQKHPITHAVTFVDNHDSPQGEALSFVQSWFKPLAYALILTRE 360
 DB 301 snsggydmrnlngsvqkhpithavtfvndhdsqpgealesfvqswfkplayalvltre 360

QY 361 QGYPVSFYGDYIGIPHGVPSSMKSDPLLQARQTYAYGTQHDYFDHDIIGWTREGDSS 420
 DB 361 qgypsfygydygipthgvpamksldpllqarqtaygtqhdyfddhdiigwtregss 420

QY 421 HPNSGLATIMSDGPGCKNMYCKHKAGQVWRDITGNRSCTVTINADGNGFTVNGGAVS 480
 DB 421 hpnsglatimsdpgpgknmygknkagqvwrditgnrtgtvtinadgngftsvnggavs 480

QY 481 VVVKQ 485
 DB 481 vvvkq 485

RESULT 7
 AAY15415
 ID AAY15415 standard; protein; 485 AA.
 XX AC AAY15415;
 XX DT 22-JUL-1999 (first entry)
 XX DE Bacillus strain NCIB 12512 alpha-amylase protein.
 XX KW Termamyl-like; alpha-amylase; variant; washing; dishwashing;
 KW production; sweetener; ethanol; starch; textile desizing;
 KW starch liquefaction; saccharification process.
 XX OS Bacillus sp.
 XX PN WO9923211-A1.
 XX PD 14-MAY-1999.
 XX PF 30-OCT-1998; 98WO-DK00471.
 XX PR 14-JUL-1998; 98DK-0000936.
 XX PR 30-OCT-1997; 97DK-0001240.
 XX PA (NOVO) NOVO-NORDISK AS.
 XX PI Andersen C, Borchert TV, Kjaerulff S, Nielsen BR;
 PI Nissen TL, Svendsen A;
 XX WPI; 1999-326987/27.
 XX New Termamyl-like alpha-amylase variants
 PS Claim 38; Page 77-79; 115pp; English.

The specification describes termamyl-like alpha-amylase variants that have altered amino acid sequences to improve properties. The variants are produced by creating one or more of the following mutations in amino acid sequence of the parent termamyl-like alpha-amylase: T141, K142, F143, D144, F145, P146, G147, R148, G149, Q174, R181, G182, D183, G184, K185, A186, W189, S193, N195, H107, K108, G109, D166, W167, D168, Q169, S170, R171, Q172, F173, F267, W268, K269, N270, D271, L272, G273, A274, L275, K311, E346, K385, G456, K457, K458, P459, G460, T461, V462, T463. The variants can be used for washing and/or dishwashing. They can also be used in the production of sweeteners and ethanol from starch, and/or for textile desizing, and in starch liquefaction and/or saccharification processes. The present amylase can function as the parent sequence in the production of the variants of the invention.

SQ Sequence 485 AA;

Query Match 96.3%; Score 2613; DB 20; Length 485;
 Best Local Similarity 95.1%; Pred. No. 9.3e-211;
 Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

QY 1 HNGTNGTMMQYFEWHLPNDSGNHNRRLDDAANLKSIGITAVWIPPAWKTSONDYGCGA 60
 DB 1 hngtngtmmqyfewlylpndgnhnrlddaaanksgitavwippawkgtsqndvggga 60

QY 61 YDLYDLGEFNQKGTVRTKYGTSRQLOGAVTSLKNNGIQVYGVDMNHKGGADGTEWNAV 120
 DB 61 yldylgefnqgtvrtkygtrnqlqaavtslknngiqvgdvmmhkggadgteivnav 120

QY 121 EVNRSNRNOEISGEYTIKAWTKFDFPGRGNTHSNFKRWYHFDGTQDQSRQONKIYKF 180
 DB 121 evnrsnrnqetsgeyaaleawtkfdfpgrgnhssfkwyhfdgtwdgsrqlqnkiyxf 180

QY 181 RGTGKAWDEVDIENGNDYLYMADIDMDHPEVINELRNWGVWYTNLNLDFRIDAVKH 240
 DB 181 rgtgkawdevdtengndylymadvdmhpevihelrnwgvwytnlnldgfridavkh 240

QY 241 IKYSYTRDMLTHVRNTGKPMFAVAEFWKNDLAAIENYLNKTSWNHSDVDFVPLHYNLYNA 300
 Db 241 ikysfrtdwltvtrnttgkpmfavaefwknldgalenylnktswnhsvdfvplhynlyna 300
 QY 301 SNSGGYFDMRNILNGSVVQKHPIHATVFDVNDHSDQGEALSFVQSWFKPLAYALILPRE 360
 Db 301 snsnggydmrnlngsvvqkhpithatvfdvndhspgealesfvqswfkplayalilpre 360
 QY 361 QGYPSVFYGDYGIPTHGVPMSKSIDPLQAROTYAYGTOHDYFDHDDIIGWTRGESS 420
 Db 361 qgypsvfgydygipthgvpamksidpllqarqtfaigtqchdyfdhddiligtregness 420
 QY 421 HPNSGLATIMSDGPGGNKMYVYGVKHKAGQVWRDITCNRSCTVTINADGNGNFTVNGGAVS 480
 Db 421 hpnsghlatimsdpggnkmyvvgknagqvwrtditgnrtgtvtinadgngnfsvnggavs 480
 QY 481 VVWKQ 485
 Db 481 vvwkq 485

RESULT 8
 AAY15421
 ID AAY15421 standard; protein; 485 AA.
 XX AC AAY15421;
 XX DT 22-JUL-1999 (first entry)
 XX DE Termamyl-like alpha-amylase protein.
 XX KW Termamyl-like; alpha-amylase; variant; washing; dishwashing;
 KW production; sweetener; ethanol; starch; textile desizing;
 KW starch liquefaction; saccharification process.
 XX OS Bacillus sp.
 XX PN WO9923211-A1.
 XX PD 14-MAY-1999.
 XX PF 30-OCT-1998; 98WO-DK00471.
 XX PR 14-JUL-1998; 98DK-0000936.
 XX PR 30-OCT-1997; 97DK-0001240.
 XX FA (NOVO) NOVO-NORDISK AS.
 XX PI Andersen C, Borchert TV, Kjaerulff S, Nielsen BR;
 PI Nissen TL, Svendsen A;
 XX DR WPI; 1999-326987/27.
 XX FT New Termamyl-like alpha-amylase variants
 XX PS Claim 38; Page 88-89; 115pp; English.

The specification describes termamyl-like alpha-amylase variants that have altered amino acid sequences to improve properties. The variants are produced by creating one or more of the following mutations in amino acid sequence of the parent termamyl-like alpha-amylase: T141, K142, F143, D144, F145, P146, G147, R148, G149, Q174, R181, G182, D183, G184, K185, A186, W189, S193, N195, H107, K108, G109, D166, W167, D168, Q169, S170, R171, Q172, F173, F367, W268, K269, N270, L271, L272, G273, A274, L275, K311, E346, K385, G456, N457, K458, P459, G460, T461, V462, T463. The variants can be used for washing and/or dishwashing. They can also be used in the production of sweeteners and ethanol from starch, and/or for textile desizing, and in starch liquefaction and/or saccharification processes. The present amylase can function as the parent sequence in the production of the variants of the invention.

Sequence 485 AA;

Query Match 96.3%; Score 2613; DB 20; Length 485;
 Best Local Similarity 95.1%; Pred. No. 9.3e-211;
 Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

QY 1 HHNGTNGTMMQYFEHLPNDGNHNRLLRDAANKLSKIGTAVWIPPAWKGTSQNDVGYGA 60
 Db 1 hhngtngtmmqyfehwlpndgnhnrllrddaanlkskigtavwippawkgsqndvgyga 60
 QY 61 YLDYDLGSEFNQKGTVRTKYGTRSQLOGAVTSLKNNIGIOVYGVVNNHKGAGDGTENVNAV 120
 Db 61 yldydlgefnqkgtvrtkygtrnqlqaavtslkongiqvgydvvmnhkggagdtainav 120
 QY 121 EVNSNRNQEISGEYTIKAWTKFDFPGRGNTSHNFKRWYHFDGTDQSQQLQNKIYKF 180
 Db 121 evnsnrnqetsgeyaieawtkfdpgrgnhshfkrwyhfdgtwdqsrqlgnkiykf 180
 QY 181 RGTGKANDWEVDIENGNYDLYMAYADIDMDHPEVINELRNMGVWYTNLTLDGFRIDAVKH 240
 Db 181 rgtgkandwevdtengnydylmyadvdmhpeviheirnwgyvtyntlnlogfridavkh 240
 QY 241 IKYSYTRDMLTHVRNTGKPMFAVAEFWKNDLAAIENYLNKTSWNHSDVDFVPLHYNLYNA 300
 Db 241 ikysfrtdwltvtrnttgkpmfavaefwknldgalenylnktswnhsvdfvplhynlyna 300
 QY 301 SNSGGYFDMRNILNGSVVQKHPIHATVFDVNDHSDQGEALSFVQSWFKPLAYALILPRE 360
 Db 301 snsnggydmrnlngsvvqkhpithatvfdvndhspgealesfvqswfkplayalilpre 360
 QY 361 QGYPSVFYGDYGIPTHGVPMSKSIDPLQAROTYAYGTOHDYFDHDDIIGWTRGESS 420
 Db 361 qgypsvfgydygipthgvpamksidpllqarqtfaigtqchdyfdhddiligtregness 420
 QY 421 HPNSGLATIMSDGPGGNKMYVYGVKHKAGQVWRDITCNRSCTVTINADGNGNFTVNGGAVS 480
 Db 421 hpnsghlatimsdpggnkmyvvgknagqvwrtditgnrtgtvtinadgngnfsvnggavs 480
 QY 481 VVWKQ 485
 Db 481 vvwkq 485

RESULT 9
 AAY07381
 ID AAY07381 standard; protein; 485 AA.
 XX AC AAY07381;
 XX DT 16-JUL-1999 (first entry)
 XX DE Wild type Termamyl(RTM)-like alpha-amylase protein #1.
 XX KW Variant: Termamyl; alpha-amylase; mutation; Bacillus; detergent;
 KW dishwashing; laundry; textile; desizing; starch liquefaction;
 XX OS sweetener; ethanol.
 XX OS Bacillus sp.
 XX Key Location/Qualifiers
 XX FH Misc-difference 181.184
 XX FT Misc-difference 195
 XX FT Misc-difference 195
 XX FT Misc-difference 206
 XX FT Misc-difference 212
 XX FT Misc-difference 216
 XX FT Misc-difference 216

"/note="optionally altered to any amino acid except an Asn residue"
 "/note="optionally altered to any amino acid except a Val residue"
 "/note="optionally altered to any amino acid except a Glu residue"
 "/note="optionally altered to any amino acid"

FT Misc-difference 269 except a Glu residue*
FT /note= *optionally altered to any amino acid
FT except a Lys residue*
XX

PN WO9919467-A1.

XX 22-APR-1999.

XX 13-OCT-1998; 98WO-DK00444.

XX 13-OCT-1997; 97DK-0001172.

XX (NOVO) NOVO-NORDISK AS.

XX Bisgard-Frantzen H, Borchert TV, Svendsen A;

DR WPI; 1999-277632/23.

XX Variant alpha-amylases - useful as detergents or for textile
PT desizing or starch liquefaction

XX Claim 1; Page 61-63; 93pp; English.

CC This sequence represents the parent sequence for new variants of a
CC parent Termamyl-like alpha-amylase with alpha-amylase activity. The
CC variants comprise mutations in 2-6 regions/positions relative to an
CC alpha-amylase from either of two Bacillus species in WO9526397,
CC B. stearothermophilus, B. licheniformis, B. amyloliquefaciens or
CC Bacillus sp. #707. The alpha-amylase variants are detergent additives
CC for use in detergents for dishwashing, manual or automatic laundry.
CC The variants can also be used for textile desizing or starch
CC liquefaction (e.g. for production of sweeteners or ethanol).

XX Sequence 485 AA;

Query Match 96.3%; Score 2613; DB 20; Length 485;
Best Local Similarity 95.1%; Pred. No. 9.3e-211;
Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

QY 1 HHNGTNGTMMQYFEWHLPNNDGNHWNRLRDDAANKSKGITAVWIPPAAWKGTSONDVGCGA 60

DB 1 hngtngtmmqyfewylpndgnhwnrlrddaanlkskgitavwippawkgtsqndvggga 60

QY 61 YDLYDLGEFNOKGTVRTKYGTRSOLOGAVTSLKNGIQYVDVVMNHKGGADGTEMVNAV 120

DB 61 ydlydlgefngkgtvrtkygtrnqlqaavtSLKngiqyvgdvvmnhkggadgclvnav 120

QY 121 EVNRSNRNOEISGEYTIETAWTKFDFGCGNTHSNFKRWYHFDGTDWQSRQLQNKIYKF 180

DB 121 evnrsnrnqetsgeyaieawtkfdfggrgnhssfkwrwyhfdgtwdqsrqlqnkikf 180

QY 181 RGTGKAWDWEVDIENGNYDYLMTADIMDHPVINELRNKGWVWYTNLTLDGFRIDAVKH 240

DB 181 rgtgkawdwevdtengnydylmyadvdmhdpeviheirnwgvwytnltldgfridavkh 240

QY 241 IKYSYTRDLTHVRNTTGKPMFAVAFKNDLAAIENYLNKTSWNHSDVDFPLHYLYNA 300

DB 241 ikysfrdlthvrntctgkpmfavaefwkdigalenylnktswnhsvfdvplhylyna 300

QY 301 SNSGGYFDNRNILNGSVQKHPIHAVTFVDNHDSPQGEALSFQSWFKPLAYALILTRE 360

DB 301 snsnggydnamrlngsvqkhphtvartvdnhdspqgealesfvqwfplayalvltre 360

QY 361 QGYPSVFYGDYIGIPTHGVPSMKSIDPLQARQTYAGTQHDYDFDHDHDIIGTREGDSS 420

DB 361 qgypsvfgydyigipthgvpamksidpllqarqtfaigtqdyfhdhdiigtreghss 420

QY 421 HPNSGLATIMSDGPGGNKMYGCKHKAGQVWRDITGNRSCTVTINADGKGNFTVNGGAVS 480

DB 421 hpnsglatimsdpgpggnkmyvgknkagqvrwditgnrtgtvtinadgwnfsvngsgvs 480

QY 481 VVVKQ 485

DB 481 vvvkq 485

RESULT 10

AAY07391

XX AAY07391 standard; Protein; 485 AA.

XX AAY07391;

XX 16-JUL-1999 (first entry)

XX Wild type Termamyl(RTM)-like alpha-amylase protein #7.

XX Variant; Termamyl; alpha-amylase; mutation; Bacillus; detergent;
KW dishwashing; laundry; textile; desizing; starch liquefaction;
KW sweetener; ethanol.

XX Bacillus sp.

XX WO9919467-A1.

XX 22-APR-1999.

XX 13-OCT-1998; 98WO-DK00444.

XX 13-OCT-1997; 97DK-0001172.

XX (NOVO) NOVO-NORDISK AS.

XX Bisgard-Frantzen H, Borchert TV, Svendsen A;

XX WPI; 1999-277632/23.

XX Variant alpha-amylases - useful as detergents or for textile
PT desizing or starch liquefaction

XX Disclosure; Page 72-74; 93pp; English.

CC This sequence represents the parent sequence for new variants of a
CC parent Termamyl-like alpha-amylase with alpha-amylase activity. The
CC variants comprise mutations in 2-6 regions/positions relative to an
CC alpha-amylase from either of two Bacillus species in WO9526397,
CC B. stearothermophilus, B. licheniformis, B. amyloliquefaciens or
CC Bacillus sp. #707. The alpha-amylase variants are detergent additives
CC for use in detergents for dishwashing, manual or automatic laundry.
CC The variants can also be used for textile desizing or starch
CC liquefaction (e.g. for production of sweeteners or ethanol).

XX Sequence 485 AA;

Query Match 96.3%; Score 2613; DB 20; Length 485;
Best Local Similarity 95.1%; Pred. No. 9.3e-211;
Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

QY 1 HHNGTNGTMMQYFEWHLPNNDGNHWNRLRDDAANKSKGITAVWIPPAAWKGTSONDVGCGA 60

DB 1 hngtngtmmqyfewylpndgnhwnrlrddaanlkskgitavwippawkgtsqndvggga 60

QY 61 YDLYDLGEFNOKGTVRTKYGTRSOLOGAVTSLKNGIQYVDVVMNHKGGADGTEMVNAV 120

DB 61 ydlydlgefngkgtvrtkygtrnqlqaavtSLKngiqyvgdvvmnhkggadgclvnav 120

QY 121 EVNRSNRNOEISGEYTIETAWTKFDFGCGNTHSNFKRWYHFDGTDWQSRQLQNKIYKF 180

DB 121 evnrsnrnqetsgeyaieawtkfdfggrgnhssfkwrwyhfdgtwdqsrqlqnkikf 180

QY 181 RGTGKAWDWEVDIENGNYDYLMTADIMDHPVINELRNKGWVWYTNLTLDGFRIDAVKH 240

DB 181 rgtgkawdwevdtengnydylmyadvdmhdpeviheirnwgvwytnltldgfridavkh 240

QY 241 IKYSYTRDMLTHVRNTTGKPMFAVAFWKNDLAAIENYLNKTSWNHNSVFDVPLHYNLYNA 300
 Db 241 ikysftrdwlthvrnttgkpmfavaefwknldgaieinylnktswnhnsfvdpplhynlyna 300

QY 301 SSSGGYFDMRNILNGSVVQKHPITHAVTEVDNHDSDQCEALESFVQSWFKPLAYALITRE 360
 Db 301 sssggydmrnilingssvvqkhpithavtevdnhdsgqcealesfvqswfkplayalvtre 360

QY 361 QGYPSVFYGDYGIPTHGVPMSKSIDPLQARQTYAYGTQHDYFDHDDIIGWTRGDS 420
 Db 361 qgypsvfgydygipthgvpamksidpllqarqtfaigtqhdqfahddiigwtrgds 420

QY 421 HPNSGLATIMSDGPGGNKMYVGHKKGAGQVWRDITGNRSGTIVTINADGNGFTVNGGVS 480
 Db 421 hpnsglatimsdpgpggnkmyvgkhkgagvwrtditgnrtgtvtinadgngftsvnggsvs 480

QY 481 VWVKQ 485
 Db 481 vwvkq 485

RESULT 11
 AAY99602
 ID AAY99602 standard; Protein; 485 AA.
 AC AAY99602;
 DT 04-SEP-2000 (first entry)
 XX Bacillus parent Termamyl-like alpha-amylase #1.
 XX Bacillus; alpha-amylase; washing; textile desizing;
 KW starch liquefaction; saccharification; mutein; mutant;
 KW enzyme stability; hybrid.
 OS Bacillus sp.
 XX WO200029560-A1.
 XX 25-MAY-2000.
 XX 16-NOV-1999; 99WO-DK00628.
 XX 16-NOV-1998; 98DK-0001495.
 XX (NOVO-) NOVO-NORDISK AS.
 XX Svendsen A, Kjaerulff S, Bisgard-Frantzen H, Andersen C;
 XX WPI; 2000-387777/33.
 XX N-PSDB; AAA48480.
 XX Variant of parent termamyl-like alpha amylase useful for washing,
 PT textile desizing and starch liquefaction, comprising alterations in one
 PT or more solvent exposed amino acid residues -
 XX Claim 8; Page 53-54; 80pp; English.
 XX The present sequence is a parent Termamyl-like alpha-amylase
 CC from which mutants with increased stability at acidic pH, low calcium
 CC concentration and high temperatures have been derived. The sequence
 CC encoding this protein was isolated from a Bacillus genomic DNA library.
 CC A variant may contain mutations in one or more solvent exposed amino
 CC acid residues to increase the overall hydrophobicity of the enzyme or the
 CC overall number of methyl groups in the side chains of exposed residues
 CC may be increased. The mutations can be incorporated by site-directed
 CC mutagenesis or by random mutagenesis. As a result of their increased
 CC stability, the variants are suitable for the industrial processing of
 CC starch, i.e. starch liquefaction and saccharification. They may also be
 CC useful for washing, dishwashing and textile desizing. Hybrid
 CC alpha-amylases comprising partial amino acid sequences derived from two
 CC or more alpha-amylases have also been created in order to increase
 CC enzyme stability.

XX SQ Sequence 485 AA;
 Query Match 96.3%; Score 2613; DB 21; Length 485;
 Best Local Similarity 95.1%; Pred. No. 9.3e-211;
 Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

QY 1 HHNGTNGTMMQYFEHLLNDGNHNRLLRDDAANLKSIGTAVWIPPAWKGTSONDVGYGA 60
 Db 1 hningtngtmmqyfewllpndgnhnrllrddaanlksigitaavwippawkgtsqndvgyga 60

QY 61 YDLYDLGFEFNOKGTVRTKYGTRSOLOQAVTSLKNNGIQVYGDVVMNHKGGADGTEMVNAV 120
 Db 61 yldydlgfefnokgtvrtkygtrsolqavtslknnigiqvygdvmmnhkggadgteivnav 120

QY 121 EVNRSNRNQEISGEYTIKAWTKFDPGGRNTHSNFKRWYHFDGTDWDSROLQNKIYKF 180
 Db 121 evnrsnrnqetsgeyaieawtkfdpggrgnhssfkwrwyhfdgtdwdsrqlqpkikykf 180

QY 181 RGTGKAWDEVDIENGNYDYLMIYADIDMDHPEVINELRNHWGWTNTLNLDGFRIDAVKH 240
 Db 181 rgtgkawdewdtenydyimiyadvmdhpevinelnrhwgwtntlnldgfridavkh 240

QY 241 IKYSYTRDMLTHVRNTTGKPMFAVAFWKNDLAAIENYLNKTSWNHNSVFDVPLHYNLYNA 300
 Db 241 ikysftrdwlthvrnttgkpmfavaefwknldgaieinylnktswnhnsfvdpplhynlyna 300

QY 301 SSSGGYFDMRNILNGSVVQKHPITHAVTEVDNHDSDQCEALESFVQSWFKPLAYALITRE 360
 Db 301 sssggydmrnilingssvvqkhpithavtevdnhdsgqcealesfvqswfkplayalvtre 360

QY 361 QGYPSVFYGDYGIPTHGVPMSKSIDPLQARQTYAYGTQHDYFDHDDIIGWTRGDS 420
 Db 361 qgypsvfgydygipthgvpamksidpllqarqtfaigtqhdqfahddiigwtrgds 420

QY 421 HPNSGLATIMSDGPGGNKMYVGHKKGAGQVWRDITGNRSGTIVTINADGNGFTVNGGVS 480
 Db 421 hpnsglatimsdpgpggnkmyvgkhkgagvwrtditgnrtgtvtinadgngftsvnggsvs 480

QY 481 VWVKQ 485
 Db 481 vwvkq 485

RESULT 12
 AAY99608
 ID AAY99608 standard; Protein; 485 AA.
 AC AAY99608;
 DT 04-SEP-2000 (first entry)
 XX Bacillus Termamyl-like alpha-amylase.
 XX Bacillus; alpha-amylase; washing; textile desizing;
 KW starch liquefaction; saccharification; mutein; mutant;
 KW enzyme stability; hybrid.
 OS Bacillus sp.
 XX WO200029560-A1.
 XX 25-MAY-2000.
 XX 16-NOV-1999; 99WO-DK00628.
 XX 16-NOV-1998; 98DK-0001495.
 XX (NOVO) NOVO-NORDISK AS.
 XX Svendsen A, Kjaerulff S, Bisgard-Frantzen H, Andersen C;
 XX PI

Db 121 evnsrnrnqetsgeyaieawtkfdipgrgnnhssfkwrwyhfdgtwdqsrqlgnkiykf 180
Qy 181 RGTGKAWDEYDIENGNDYLMYADIDMDHPVINELRNMGVWYTNLTNLDGFRIDAVKH 240
Db 181 rgtgkawdewdtengnydylmadvdmhpveihelrnwgvwyntnldgfridavkh 240
Qy 241 IKYSYTRDMLTHVRNTTKGPMFAVAEFWKNOLAALNIENLNTSNHVSFVDPPLHNLNA 300
Db 241 ikysftrdmlthvnrnttkgpmfavaefwknldgalenylntkswnhsvfdvplhnylna 300
Qy 301 SNSGGYFDMRNILNGSVVQKHPHIAVTFVDNHDSPGGALESFVQSWFKPLAYAILTRE 360
Db 301 snsggymrnilngsvvqkhphtavtfvdnhdspggaalesfvqswfkplayailtre 360
Qy 361 QGYPSVFYGYGIPTHGVPMSKIDPLQARQTYAYGTQHDYFDHHDIIIGWTREGDSS 420
Db 361 qgypsvfgygygipthgvpamksidpllqarqtaygtqhdhdyfdhhdiiigwtregss 420
Qy 421 HPNSGLATIMSDGPGGNKWMYVGHKAGQVWRDITGNRSCTVTINADGWGNTVNGGAVS 480
Db 421 hpnsghlatimsdpgpgnkwmyvghkagvwrdrtnrtgtvtinadgwnfsvngsgvs 480
Qy 481 VWVKQ 485
Db 481 vvwkq 485

RESULT 14
AAW12129
ID AAW12129 standard; protein: 485 AA.
XX
AC AAW12129;
XX
DT 08-APR-1997 (first entry)
XX
DE Alpha-amylase variant E190Q.
XX
KW Alpha-amylase; detergent; thermal stability; oxidation stability; enzyme;
KW calcium ion dependency; alpha-amylolytic activity; washing composition;
KW textile desizing; papermaking; beer-making; ethanol production;
KW sweetener.
XX
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Misc-difference 190
FT /label= E190Q
XX
XX W09623873-A1.
XX
XX PD 08-AUG-1996.
XX
XX PF 05-FEB-1996; 96WO-DK000056.
XX
XX PR 06-OCT-1995; 95DK-0001121.
XX PR 03-FEB-1995; 95DK-0000126.
XX PR 29-MAR-1995; 95DK-0000336.
XX PR 29-SEP-1995; 95DK-0001097.
XX
XX PA (NOVO) NOVO-NORDISK AS.
XX
XX PI Bisgard-frantzen H, Borchert T, Svendsen A;
XX
XX DR WPI; 1996-371423/37.
XX
XX PT Alpha-amylase variants - with improved thermal and oxidation
XX stability and reduced calcium ion dependency
XX
XX PS Claim 11; : 11lpp; English.
XX
XX AAW12098-W12144 represent alpha-amylase variants of the invention. The
CC variants of the invention were created using site directed, or random,
CC mutagenesis of the DNA sequences encoding the parent alpha-amylases

CC represented by AAW12955, AAW12956, AAR81835 and AAR81836.
CC AAW12098-W12136, AAW12141, AAW12142 and AAW12144 are specifically
CC variants of the alkaliphilic Bacillus strain NCIB 12512 alpha-amylase shown
CC in AAR81835. These variants can have improved thermal stability (such as
CC at temperatures in the range of 40-70 degrees Celsius), and/or oxidation
CC stability, and/or reduced calcium ion dependency. The variants can also
CC have increased alpha-amylolytic activity (especially at pH values in the
CC range of 8.5-10.5), and improved binding of a particular substrate.
CC These variant alpha-amylases also possess improved specificity to a
CC particular substrate, and/or improved specificity with respect to
CC cleavage of substrate. These sequences can be used in detergent and
CC washing compositions, and for textile desizing. The alpha-amylase
CC variants can also be used in papermaking and beer-making processes.
CC These variants can also be used in the production of sweeteners and
CC ethanol from starch.
XX
SQ Sequence 485 AA;

Query Match 96.2%; Score 2610; DB 17; Length 485;
Best Local Similarity 94.8%; Pred. No. 1.7e-210;
Matches 460; Conservative 17; Mismatches 8; Indels 0; Gaps 0;

Qy 1 HNGTNGTMMOYFEWHLPNDGNHWNRLRDDAANKLSKGITAVWIPPAWKGTSONDVGYGA 60
Db 1 hngtngcmmdyfewipndgnhwnrlrddaanlkskgitavwippawkwgtsqndvgyga 60
Qy 61 YDLXDLGEFNQKGTVRTKYGRSLOLQGAVTSLKNNGIQVYGVVNMHKGADGTEMVNAV 120
Db 61 ydylxlgefnqkgtvrtkygrnqlqaavtslknngiqvgygvnmhkggadgteivnav 120
Qy 121 EVNRSNRNQEISGEYTTIATWTKFDFPGRGNTHSNFKRWYHFDGTDWDQSRQLQNKIYKF 180
Db 121 evnrsnrnqetsgeyaieawtkfdipgrgnnhssfkwrwyhfdgtwdqsrqlgnkiykf 180
Qy 181 RGTGKAWDEYDIENGNDYLMYADIDMDHPVINELRNMGVWYTNLTNLDGFRIDAVKH 240
Db 181 rgtgkawdewdtengnydylmadvdmhpveihelrnwgvwyntnldgfridavkh 240
Qy 241 IKYSYTRDMLTHVRNTTKGPMFAVAEFWKNOLAALNIENLNTSNHVSFVDPPLHNLNA 300
Db 241 ikysftrdmlthvnrnttkgpmfavaefwknldgalenylntkswnhsvfdvplhnylna 300
Qy 301 SNSGGYFDMRNILNGSVVQKHPHIAVTFVDNHDSPGGALESFVQSWFKPLAYAILTRE 360
Db 301 snsggymrnilngsvvqkhphtavtfvdnhdspggaalesfvqswfkplayailtre 360
Qy 361 QGYPSVFYGYGIPTHGVPMSKIDPLQARQTYAYGTQHDYFDHHDIIIGWTREGDSS 420
Db 361 qgypsvfgygygipthgvpamksidpllqarqtaygtqhdhdyfdhhdiiigwtregss 420
Qy 421 HPNSGLATIMSDGPGGNKWMYVGHKAGQVWRDITGNRSCTVTINADGWGNTVNGGAVS 480
Db 421 hpnsghlatimsdpgpgnkwmyvghkagvwrdrtnrtgtvtinadgwnfsvngsgvs 480
Qy 481 VWVKQ 485
Db 481 vvwkq 485

RESULT 15
AAW12130
ID AAW12130 standard; protein: 485 AA.
XX
AC AAW12130;
XX
DT 08-APR-1997 (first entry)
XX
DE Alpha-amylase variant E194Q.
XX
KW Alpha-amylase; detergent; thermal stability; oxidation stability; enzyme;
KW calcium ion dependency; alpha-amylolytic activity; washing composition;
KW textile desizing; papermaking; beer-making; ethanol production;

KW sweetener.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 FT MISC-difference 194
 FT /label= E1940
 XX XX WO9623873-A1.
 XX XX 08-AUG-1996.
 XX PF 05-FEB-1996; 96WO-DK00056.
 XX PR 06-OCT-1995; 95DK-0001121.
 XX PR 03-FEB-1995; 95DK-0000126.
 PR 29-MAR-1995; 95DK-0000336.
 PR 29-SEP-1995; 95DK-0001097.
 XX XX (NOVO) NOVO-NORDISK AS.
 XX XX Bisgard-frantzen H, Borchert T, Svendsen A;
 XX XX WPI; 1996-371423/37.
 XX XX Alpha-amylase variants - with improved thermal and oxidation
 PT stability and reduced calcium ion dependency
 PT Claim 11; : 111pp; English.
 XX XX AAW12098-W12144 represent alpha-amylase variants of the invention. The
 CC variants of the invention were created using site directed, or random,
 CC mutagenesis of the DNA sequences encoding the parent alpha-amylases
 CC represented by AAW12955, AAW12956, AAR81835 and AAR81836.
 CC AAW12098-W12136, AAW12141, AAW12142 and AAW12144 are specifically
 CC variants of the alkalophilic bacillus strain NCIB 12512 alpha-amylase shown
 CC in AAR81835. These variants can have improved thermal stability (such as
 CC at temperatures in the range of 40-70 degrees Celsius), and/or oxidation
 CC stability, and/or reduced calcium ion dependency. The variants can also
 CC have increased alpha-amylolytic activity (especially at pH values in the
 CC range of 8.5-10.5), and improved binding of a particular substrate.
 CC These variant alpha-amylases also possess improved specificity to a
 CC particular substrate, and/or improved specificity with respect to
 CC cleavage of substrate. These sequences can be used in detergent and
 CC washing compositions, and for textile desizing. The alpha-amylase
 CC variants can also be used in papermaking and beer-making processes.
 CC These variants can also be used in the production of sweeteners and
 CC ethanol from starch.
 XX XX Sequence 485 AA;

Search completed: November 28, 2001, 16:58:05
 Job time: 208 sec

Query Match 96.2%; Score 2610; DB 17; Length 485;
 Best Local Similarity 94.8%; Pred. No. 1.7e-210;
 Matches 460; Conservative 17; Mismatches 8; Indels 0; Gaps 0;

QY 1 HHNGTNGTMQYFEWHLPPNDGNHNRLLRDAANKSKGITAVWIPPAWKCTSONDVG YGA 60
 |||||
 Db 1 hngtngtmqyfewlppndgnhnrllrddaaanksgitavwippawkgtsqndvg yga 60
 |||||

QY 61 YDLYGEGFNQKGVTRFKYTRSOLOGAVTSLKNNIGIYVYGDVVMNHKGGADGTEMYNAV 120
 |||||
 Db 61 ydlygefngkgtvrtkygtrnglqaaavtslknngiqvygddvmmnhkggagdtelvnv 120
 |||||

QY 121 EVNRNRNQEISGEYTTTEAWTKFDFGCGNTHSNFKRWYHFDGTDWDQSRQLONKIYKF 180
 |||||
 Db 121 evnrnrngetsgeyaleawtkfdfpgrgnhshsfkwrwyhfdgtdwdqsrqlgnkiykf 180
 |||||

QY 181 RGTGKAWDEVDYENGNDYLYMADIDMDHPEVINELRNKGVWYNTNTLNDGFRIDAVKH 240
 |||||
 Db 181 rgtgkawdewdvcqngnydlymadvdmhdhpevihelrnwgvwyntntcldgfridavkh 240
 |||||

QY 241 IKYSYTRDNLTHVRNTTGTGKPMFAVEFWKNDLAAIENLYLNKTSWNHSHVDFVPLHLYNA 300
 |||||

Db 241 ikysftrdrwthvrnttgkpmfavaefwkndlgaienylnktswnhsvfdvplhlyna 300
 |||||
 QY 301 SNSGGYEDMBENILNGSVVQKHPITHAVTFVDNHDSPQGEALESFVQSWFKPLAYALITRE 360
 |||||
 Db 301 snsggyddmrnilngsvvqkhpthavtfvdnhdspqgealesfvqwkplayalvitre 360
 |||||
 QY 361 QGYPSVFYGYDYGIPTHGVPMSKSKIDPLQAROTYAYGTQHDYFDHHDIIIGWTREGDSS 420
 |||||
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; LENGTH: 1455 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-861-837-5

alignment_scores:
  Quality: 1860.50      Length: 483
  Ratio: 4.327          Gaps: 2
Percent Similarity: 89.027 Percent Identity: 66.460

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17 nAspGlyGlnHisTrpAsnArgLeuHisAspAspAlaAlaLeuSera 34
57 TGATGGGAATCACTGGAATAGATTAAGAGATGATGCTAGTAATCTAAGAA 106
34 sAlaGlyIleThrAlaIleTrpPleProAlaTyrLysGlyAsnSer 50
107 ATAGAGGTATACCGCTATTGGATTCCGCCCTGCCCTGGAAAGGACTTCG 156
51 GlnAlaAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuGlyLuph 67
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67 eAsnGlnLysGlyThrValArgThrLysTyrGlyThrLysAlaGlnLeuG 84
207 TAAATCAAAAGGGGAGCGTTCCGTACTAAGTATGGGACACGTAGTCAATTGG 256
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257 AGCTGCCATCCATCTTTAAGAATAATGGCGTTCAAGCTTTATGGGGAT 306
101 ValValMetAsnHisLysMetGlyAlaAspPheThrGluAlaValGlnAl 117
307 GTAGTGATGAACCAATAAGGAGGAGCTGATGCTACAGAAACGTTCTTGC 356
117 aValGlnValAsnProThrAsnArgTrpGlnAspIleSerGlyAlaTyrT 134
357 TGTGAGGTGAATCCAAATACCGGAATCAAGAAATATCTGGGGAGCTACA 406
134 hrIleAspAlaTrpThrGlyPheAspPheSerGlyArgAsnAsnAlaTyr 150
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507 ATCAGACAATTTCCAAAATCGTATCTACAAATTCGAGGTGATGGTAAGG 556
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198 GlySerAsnIleAspPheSerHisProGluValGlnAspGluLeuLysAs 214
607 TATGCAGATGTAGATATGATCATCCGGAGGTAGTAATAGCTTAGAAG 656
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seq_documentation_block:
; Sequence 5, Application US/08600656
; Patent No. 6093562
; GENERAL INFORMATION:
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: AMYLASE VARIANTS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:

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448 aspLeuThrGlyAsnAsnGlyAlaSerValThrIleAsncllyAspGlyTr 464
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464 pGlyGluPheThrAspGlyClySerValSerValTyrValAsnGln 480
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1407 GGCTAAATTTTTTCAGTAAATGGAGGATCTGTTCCATTTGGGTGAACGA 1455
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407 CAATTGAGGCTTGGCAATAAGTTTGAATTTCCAGGAGGGGTAATACATAC 456
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seq_documentation_block:
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; Patent No. 6187576
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgaard-Frantzen Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 5276.200-US
; CURRENT APPLICATION NUMBER: US/09/170,670
; CURRENT FILING DATE: 1998-10-13
; EARLIER APPLICATION NUMBER: 1172/97
; EARLIER FILING DATE: 1997-10-13
; EARLIER APPLICATION NUMBER: 60/063,306
; EARLIER FILING DATE: 1997-10-28
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 1455
; TYPE: DNA
; ORGANISM: Bacillus sp.
US-09-170-670-15

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Ratio: 4.327 Gaps: 2
Percent Similarity: 89.027 Percent Identity: 66.460

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34 spAlaGlyIleThrAlaIleTrpIleProAlaTyrLysGlyAsnSer 50
107 ATAGAGGTATACCGCTATTGGATTCCGCTGCCCTGGAAAGGAGCTTCG 156
51 GlnAlaAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuGlyGluPh 67
157 CAAATATGATGTGGGTATGGAGCCATGATCTTTATGATTTAGGGAAT 206
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; Sequence 14, Application US/09193068
; Patent No. 6197565
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Kjruliff, S ren
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Andersen, Carsten
; TITLE OF INVENTION: -Anyase Variants
; FILE REFERENCE: 5709.000-US
; CURRENT APPLICATION NUMBER: US/09/193,068
; CURRENT FILING DATE: 1998-11-16
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 1455
; TYPE: DNA
; ORGANISM: Bacillus sp.
US-09-193-068-14
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seq_documentation_block:
; Sequence 10, Application US/09183412
; Patent No. 6204232
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben V.
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nissen, Torben L.
; APPLICANT: Kjaerulff, Soren
; TITLE OF INVENTION: Alpha-Amulase Mutants
; FILE REFERENCE: 5368.200-US
; CURRENT APPLICATION NUMBER: US/09/183.412
; CURRENT FILING DATE: 1998-10-30
; EARLIER APPLICATION NUMBER: 60/064,662
; EARLIER FILING DATE: 1997-11-06
; EARLIER APPLICATION NUMBER: 60/093,234
; EARLIER FILING DATE: 1998-07-17
; EARLIER APPLICATION NUMBER: 1240/97
; EARLIER FILING DATE: 1997-10-30
; EARLIER APPLICATION NUMBER: PA 1998 00936
; EARLIER FILING DATE: 1998-07-14
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 1455
; TYPE: DNA
; ORGANISM: Bacillus sp.
US-09-183-412-10
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Percent Similarity: 89.027 Percent Identity: 66.460
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67 eAsnGlnLysGlyThrValArgThrLysTyrGlyThrLysAlaGlnLeuG 84
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101 ValValMetAsnHisLysMetGlyAlaAspPheThrGluAlaValGlnAl 117
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307 GTAGTGATGAACCATAAAGGAGGAGTGATGCTACAGAAAACGTTCTTGC 356
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seq_documentation block:
; Sequence 5, Application US/09354191A
; Patent No. 6297038
; GENERAL INFORMATION:
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: AMYLASE VARIANTS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6297038o No. 6297038disk of No. 6297038th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
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: ZIP: 10174-6401
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/354.191A
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/600,656
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Lambiris, Elias J.
: REGISTRATION NUMBER: 33,728
: REFERENCE/DOCKET NUMBER: 4318.204-US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 212 867 0123
: TELEFAX: 212 867 0298
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1455 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: US-09-354-191A-5

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51 GlnAlaAspValGlyIleThrAlaIleThrIleGlyAspLeuGlyGluPh 67
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157 CAGAATGATGATAGGTATAGGACCTTATGATTTATATGATCTTTGGAGATT 206

67 eAsnGlnIleGlyThrValAlaGlyThrIleGlyThrIleGlyAlaGlnLeu 84
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seq_documentation_block:
; Sequence 4, Application US/08861837
; Patent No. 5856164
; GENERAL INFORMATION:
; APPLICANT: Ottup, Helle
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Ostergaard, Peter Rahbek
; APPLICANT: Rasmussen, Michael Dolberg
; APPLICANT: Van Der Zee, Pia
; TITLE OF INVENTION: Alkaline Bacillus Amylase
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 58561640 No. 5856164disk of No. 5856164th America
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/861,837
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/446,803
; FILING DATE: 01-June-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Harrington, James J.
; REGISTRATION NUMBER: 38,711
; REFERENCE/DOCKET NUMBER: 4157,204-US
; TELECOMMUNICATION INFORMATION:
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; TELEPHONE: (212) 867-0123
; TELEFAX: (212) 878-9655
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1455 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-861-837-4

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seq documentation block:
; Sequence 4, Application US/08600656
; Patent No. 6093562
; GENERAL INFORMATION:
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Svendsen, Allan
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; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: AMYLASE VARIANTS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 60935620 No. 60935620disk of No. 60935620th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/600,656
; FILING DATE: 13-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4318.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 867 0298
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1455 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-600-656-4

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alignment_scores:
  Quality: 1835.50      Length: 483
  Ratio: 4.319          Gaps: 2
Percent Similarity: 87.992 Percent Identity: 66.253

alignment_block:
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Align seg 1/1 to: US-08-600-656-4 from: 1 to: 1455

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17 nAspGlyGlnHisTTrpAsnArgLeuHisAspAlaAlaLeuSera 34
57 TGACGGGAAATCATTTGGACAGGTTGAGGATGACCGAGCTTAAAGA 106
34 spAlaGlyLeuThrAlaLeuThrProAlaTyrProAlaTyrGlyAsnSer 50
107 GTAAAGGGATAACAGCTGTATGATGCCACCTGCATGGAAGGGACTTCC 156
51 GlnAlaAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuGlyGluPh 67
157 CAGAATGATGATAGGTATGGAGCCATGATTTATATGATGTTGGAGAGTT 206
67 eAsnGlnLysGlyThrValArgThrLysTyrGlyThrLysAlaGlnLeuG 84
207 TAACCAGAGAGGGAGGTTTCGTACAAATATATGGAACCGCAACACGCTAC 256
84 luArgAlaLeuGlySerLeuLysSerAsnAspIleAsnValTyrGlyAsp 100
257 AGGCTGGGTGACCTCTTTAAAAATAACGGCATTCAGGTATATGGTAT 306
101 ValValMetAsnHisLysMetGlyAlaAspPheThrGluAlaValGlnAl 117
307 GTGCTCATGAATCATAAAGGTGGAGCAGATGTTACGGAATTTGTAATGC 356

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117 aValGlnValAsnProThrAsnArgTyrGlnAspIleSerGlyAlaTyr 134
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134 hrIleAspAlaTyrThrGlyPheAspPheSerGlyArgAsnAlaTyr 150
407 :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
407 CAATAGAAAGCGTGGACAAAGTTGATTTTCTCTGGAAGAGAAATAACCAT 456
151 SerAspPheLysTyrArgTyrPheHisPheAsnGlyValAspTyrAspG 167
457 :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
457 TCCAGCTTTAAAGTGGCTGTATCATTTTGTGGACAGATTTGGATCA 506
167 n...ArgTyrGlnGluAsnHisIlePheArgPheAlaAsnThrAsn... 181
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182 ..TTrpAsnTyrArgValAspGluAsnGlyAsnTyrAspTyrLeuLeu 197
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807 AAATGACCTTGGTGCATTAATAAATAATTTGAATAAACAAGTTGGAATC 856
281 etSerLeuPheAspValProLeuAsnTyrAsnPheTyrArgAlaSerGln 297
857 :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
857 ACTCGTGTGTTGATGTTCTCTCCACTATATTTGTAACAATGCATCTAAT 906
298 GlnGlyGlySerTyrAspMetArgAsnIleLeuArgGlySerLeuValG 314
907 :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
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314 uAlaHisProMetHisAlaValThrPheValAspAsnHisAspThrGlnP 331
957 :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
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331 rGlyGluSerLeuGluSerTrrpValAlaAspTrrpPheLysProLeuAla 347
1007 :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
1007 CCGGGGAAGCATTTGGAATCCTTTGTTCAACAATGTTTAAACCACTTGA 1056
348 TyrAlaThrIleLeuThrArgGluGlyTyrProAsnValPheTyrG 364
1057 :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
1057 TATGATTTGGTTCTGACAGGGAACAAGTTATCTCTCGGTATTTTATGG 1106
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1107 :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
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1207 :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
1207 GATTACTTTGATCATCATGATATATTCGCTTGGACAAGAGAGGGAATAG 1256

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431 lySerLysTrpMetTyrValGlyArgGlnAsnAlaGlyGlnThrTyr 447
1307 GTAACAAATGGATGTATGGGGGAAAAATAAACGGGCAACAGTTTGAGA 1356
448 AspLeuThrGlyAsnAsnGlyAlaSerValThrIleAsnGlyAspGlyTyr 464
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464 pGlyGluPhePheThrAsnGlyGlySerValSerValTyrValAsnGln 480
1407 GGGTAATTTCTCTCTAATGAGGGTCCGTTTCGGTTTGGGTGAAGCAA 1455
seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-170-670-9

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seq_documentation_block:

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; Sequence 9, Application US/09170670
; Patent No. 6187576
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgard-Frantzen Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 5276.200-US
; CURRENT APPLICATION NUMBER: US/09/170,670
; CURRENT FILING DATE: 1998-10-13
; EARLIER APPLICATION NUMBER: 1172/97
; EARLIER FILING DATE: 1997-10-13
; EARLIER APPLICATION NUMBER: 60/063,306
; EARLIER FILING DATE: 1997-10-28
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 1455
; TYPE: DNA
; ORGANISM: Bacillus sp.
US-09-170-670-9

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alignment_scores:
  Quality: 1835.50      Length: 483
  Ratio: 4.319          Gaps: 2
  Percent Similarity: 87.992  Percent Identity: 66.253

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alignment_block:

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US-09-590-375-1 x US-09-170-670-9 ..
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Align seg 1/1 to: US-09-170-670-9 from: 1 to: 1455
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1 AspGlyLeuAsnGlyThrMetMetGlnTyrTyrGluTrpHisLeuGluAs 17
7 AATGGAACAAATGGTACTATGATGCAATATTCGAATGGTATTGGCAA 56
17 nAspGlyGlnHisTrpAsnArgLeuHisAspAlaAlaLeuSerA 34
57 TGACGGGAATCATFTGGAACAGGTTGAGGATGACGAGCTAACTTAAAGA 106
34 sPaLaGlyIleThrAlaIleTrpIleProAlaTyrLysGlyAsnSer 50
107 GTAACGGGATAACAGCTGTATGATGCCACCTGCATGGGAAGGGGACTTCC 156
51 GlnAlaAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuGlyGluPh 67
157 CAGAATGATGTAGTGTATGGAGCCTATGATTTATATGATCTTGGAGATT 206
67 eAsnGlnLysGlyThrValArgThrLysTyrGlyThrLysAlaGlnLeuG 84
207 TAACCAAGAGGGGACGGTTCGTACAAAATATGGAACACGACACGACTAC 256
84 luArgAlaIleGlySerLeuLysSerAsnAspIleAsnValTyrGlyAsp 100

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257 AGCGCTCGGTGACCTCTTTAAAAAATAACGGCATTCAGGTATATGGTGAT 306
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117 aValGlnValAsnProThrAsnArgTrpGlnAspIleSerGlyAlaTyrT 134
357 GGTAGAAGTGAATCGGGACCAACCGAAACAGGAACCTCAGGAGAGTATG 406
134 hrtIleAspAlaTrpThrGlyPheAspPheSerGlyArgAsnAlaTyr 150
407 CAATAGAAGCGTGGCAAAAGTTTGATTTTCTCGAAGAGGAAATAACCAT 456
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457 TCCAGCTTTAAGTGGCGCTGGTATCATTTTGTATGGACAGATTTGGGATCA 506
167 n...ArgTyrGlnGluAsnHisIlePheArgPheAlaAsnThrAsn... 181
507 GTCACGCCAGCTTCAAAACAAATAATATAAATTCAGGGGAACAGCAAGG 556
182 ..TrpAsnTrpArgValAspGluLysAsnGlyAsnTyrAspTyrLeuLeu 197
557 CCTGGGACTGGGAAGTCGATACAGAGAATGGCAACTATGACTATCTTATG 606
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657 CTGGGAGTGTGTATACGAATACACTGAACCTTGATGGATTTAGAATAG 706
231 sPaLaIleLysHisIleProPheTrpTyrThrSerAspTrpValArgHis 247
707 ATGCACTGAACATATAAATAATATAGCTTTACGAGAGATTTGGCTTACACAT 756
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281 etSerLeuPheAspValProLeuAsnTyrAsnPheTyrArgAlaSerGln 297
857 ACTCGGTGTTTGATGTTCTCTCCACTATAAATTTGACAATGCATCTAAT 906
298 GlnGlyGlySerTyrAspMetArgAsnIleLeuArgGlySerLeuValG 314
907 AGCGGTGGTTATATCATATGAGAAATATTTAAATGGTCTGTGTGTGCA 956
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331 roGlyGluSerLeuGluSerTrpValAlaAspTrpPheLysProLeuAla 347
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; Sequence 14, Application US/09170670
; Patent No. 6187576
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> PATENT NO.: 0107270
> GENERAL INFORMATION:
> APPLICANT: Svendsen, Allan
> APPLICANT: Borchert, Torben
> APPLICANT: Bisgard-Frantzen Henrik
> TITLE OF INVENTION: Alpha-Amylase Mutants
> FILE REFERENCE: 5276-200-US
> CURRENT APPLICATION NUMBER: US/09/170.670
> CURRENT FILING DATE: 1998-10-13
> EARLIER APPLICATION NUMBER: 1172/97
> EARLIER FILING DATE: 1997-10-13
> EARLIER APPLICATION NUMBER: 60/063.306
> EARLIER FILING DATE: 1997-10-28
> NUMBER OF SEQ ID NOS: 22
> SOFTWARE: fastseq for Windows Version 3.0
> SEQ ID NO 14
> LENGTH: 1455
> TYPE: DNA
> ORGANISM: Bacillus sp.
> US-09-170-670-14

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alignment_scores:
  Quality: 1835.50      Length: 483
  Ratio: 4.319          Gaps: 2
  Percent Similarity: 87.992  Percent Identity: 66.253

alignment_block:
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  Align seg 1/1 to: US-09-170-670-14 from: 1 to: 1455

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7  AATGGACAATGGTACTATGATGCAATATTTTCSAATGGTATTTCGCAAA 56
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17 nAspGlyGlnHisTrpAsnArclLeuHisAspAspAlaAlaLeuSerA 34
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57 TGACGGGAATCATGTGGAACAGGTTGAGGATGACCGCAGCTTAACCTAAAGA 106
   |||||:::| | | | | | | | | | | | | | | | | | | | | | | |

34 sPalacGlyIleThrAlaIleTrpIleProProAlaTyrLysGlyAsnSer 50
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107 GTAAAGGGATAACACAGCTGTATGATGCCACCTGTCATGGAAGGGAGCTTC 156
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51 GlnAlaAspValcIlyTyrGlyAlaTyrAspLeuTyrAspLeuGlyGluPh 67
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157 CAGATGATGTAGGTTATGAGCGCTATGATTATATGATGATCTTCGAGATT 206
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/SIDS2/gcgdata/geneseq/NA1996.DAT:AAT32228	/SIDS2/gcgdata/geneseq/NA1996.DAT:AAT32228	1723.50	2891.41	4.6e-153	1593
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/SIDS2/gcgdata/geneseq/NA1997.DAT:AAT74272	/SIDS2/gcgdata/geneseq/NA1997.DAT:AAT74272	1723.50	2889.73	7.0e-153	1893
/SIDS2/gcgdata/geneseq/NA1997.DAT:AAT77063	/SIDS2/gcgdata/geneseq/NA1997.DAT:AAT77063	1723.50	2889.73	7.0e-153	1893
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353 ATGCTGGTATTACAGCTATTGGGATTCGCCAGGCTACAAAGGTAATAGT 402
51 GlnAlaAspValGlyTyrGlyAlaIleTrpAspLeuValGlyGluPh 67
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403 CAGCGGATTTGGGTGCGTACGATGATCTTTATGATTTAGGAGATT 452
67 eAsnGlnLysGlyThrValArgThrLysTyrGlyThrLysAlaGlnLeu 84
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seq_documentation_block:
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XX
AC AAA70313;
XX
DT 19-DEC-2000 (first entry)
XX
DE Bacillus sp. liquefying alpha-amylase #1 coding sequence.
XX
KW Liquefying alpha-amylase; detergent; starch industry; brewing industry;
KW pharmaceutical industry; food industry; fibre industry; ds.
XX
OS Bacillus sp.
XX
FH Key Location/Qualifiers
CDS 65..1570
FT /*tag= a
FT /product= "alpha-amylase"
XX
PN EPI022334-A2.
XX
PD 26-JUL-2000.
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PF 20-DEC-1999; 99EP-0125399.
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PR 21-DEC-1998; 98JP-0362487.
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PR 21-DEC-1998; 98JP-0362488.
XX
PA (KAOS ) KAO CORP.
XX

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PI Hagihara H, Kitayama K, Hayashi Y, Igarashi K, Endo K, Ozaki K;
 XX WPI: 2000-516014/47.
 DR P-PSDB; AAB14821.
 DR
 XX New liquefying alkaline amylase, useful in a detergent composition
 PT comprises a residual activity of not less than 70 % when treated under
 PT specific conditions -
 PT
 XX Claim 6; Page 20-23; 34pp; English.
 PS
 XX The present sequence is the coding sequence of a novel alpha-amylase from
 CC Bacillus sp. The invention concerns the isolation of two new liquefying
 CC alpha-amylases (and their coding sequences) from Bacillus sp. strains
 CC KSM-K36 and KSM-K38, designated K36 and K38, of which this sequence
 CC encodes one. The alpha-amylases of the invention are chelating-agent
 CC resistant and thus are useful in the starch, brewing, fibre,
 CC pharmaceutical and food industries, and especially as components of
 CC detergents.
 XX
 SQ Sequence 1650 BP; 475 A; 267 C; 420 G; 488 T; 0 other;

alignment_scores:
 Quality: 2618.00 Length: 480
 Ratio: 5.477 Gaps: 0
 Percent Similarity: 99.583 Percent Identity: 96.458

alignment_block:
 US-09-590-375-1 x AAA70313 ..

Align seg 1/1 to: AAA70313 from: 1 to: 1650

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957 ACGTCATCCGAGCGGCTGCGTTACGTTTGTGATACCCAGCACACACAGC 1006
331 roGlyGluSerLeuGluSerTrpValAlaAspTrpPheLysProLeuAla 347
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XX AC AA00777;
XX DT 16-MAR-1996 (first entry)
XX DE Bacillus sp. alkaline alpha-amylase DNA.
XX KW Alpha-amylase; enzyme; EC-3.2.1.1; detergent; surfactant; textile;
XX OS beer; starch; ss.
XX PN Bacillus.
XX PR WO9526397-Al.
XX PD 05-OCT-1995.
XX PF 29-MAR-1995; 95WO-DK00142.
XX PR 03-FEB-1995; 95DK-0000123.
XX PR 29-MAR-1994; 94DK-0000353.
XX PR 03-NOV-1994; 94DK-0001271.
XX PA (NOVO ) NOVO-NORDISK AS.
XX PI Bisgard-frantzen H, Ostergaard PR, Outtrup H, Rasmussen MD;
XX PI Van DER ZEE P;
XX DR WPI; 1995-351318/45.
XX PT New alkaline Bacillus alpha-amylase - used in e.g. detergent
XX PT compns. starch liquefaction, textile desizing, starch modification
XX PT or beer making
XX PS Disclosure; Page 50; 65pp; English.
XX CC This DNA sequence may be expressed recombinantly for the production
XX CC of an alpha-amylase protein. The produced protein is characterized
XX CC by having a specific activity at least 25% higher than the specific
XX CC activity of Termamyl at 25-55 deg C and a pH of 8-10. The enzyme
XX CC can be used in detergent composition for starch liquefaction, the
XX CC production of lignocellulosic materials, e.g. pulp, paper and
XX CC cardboard from waste containing starch, for deinking recycled
XX CC starch-coated, or starch- containing printed paper, to modify

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CC starch for papermaking, for textile desizing, and beer-making
CC processes.

Sequence 1455 BP; 473 A; 228 C; 351 G; 403 T; 0 other;
XX
SQ

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Ratio:	4.334	Gaps: 2
Percent Similarity:	89.027	Percent Identity: 66.667

alignment_block:

US-09-590-375-1 x AAT00777

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17 nAspGlyGlnHisTrpAsnArgLeuHisAspAspAlaAlaLeuSera 34
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151 SerAspPheLysTrpArgTrpPheHisPheAsnGlyValAspTrpAspG1 167
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314 ualaHisPromethisAlavalThrPheValaspasnHisaspthrglnp 331  
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957 AAGACATCAATGCATGCCGTAACTTTTTGTGGATAATCACGATTCCTCAAC 1006  
331 roglyGluSerLeuGluSerTripValAlaAspTrpPhelysProLeuAla 347  
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1007 CTGGGGAAATCATTAGAATCATTTGTACAGAATGGTTTAAACCACCTGCT 1056  
348 TyrAlaThrIleLeuthrArgGluGlyGlyTyrProAsnValPheYrGl 364  
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1057 TATGCCCTTATTTTAAACAGAGAACAAGGCGTATCCCTCTGCTTCCTATGG 1106  
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1107 TGACTACTATGGAATTTCCAACACATAGTGTCCCAGCAATGAAGCCCAAGA 1156  
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1157 TTGATCCATCTTAGAGGCCGTCAAAATTTGCATATGGAACACACACAT 1206  
398 AspTyrPheAsphistrpsavvalvglytrpthrargGluGlyserse 414  
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1207 GATTATTTTGACCATCATATAATAATCGGATGGACACGTGAAGGAAATAC 1256  
414 rSerArgProAsnSerGlyLeualathrilemetSerAsnGlyprocgly 431  
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1257 CAGCGATCCCAATTCAGGACTTCGGACTATCATGTGCGATGGCCGACGGG 1306  
431 lySerlystrpmettyrvalglyyargGlnAsnalaglyGlnThrTrpThr 447  
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seq documentation block:

seq_documentation_block:
ID AAX59633 standard: DNA: 1455 BP.

XX
AC
AA59633.XX
DT 22-III-1999 (first entry)

XX DNA encoding a + ornamental = 14

XX

KW production; sweetener; ethanol; starch; textile desizing;
KW starch liquefaction; saccharification process; ss.

248 GlnArgAsnGluAlaAspGlnAspLeuPheValValGlyGluTyrTrpLy 264
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PD 757 GTAAGAACCGCAACGGGAAAGAAAGATGTTCTGCTGCTGAATTTGGAA 806
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XX 264 SASAspValGlyAlaLeuPheTyrLeuAspGluMetAsnTrpGluM 281
XX ||||||| :
XX 807 AAATGATTTAGTGCCTTGGAGAACTATTAAATAAACAACACTGGGAATC 856
XX ||||||| :
XX 281 etSerLeuPheAspValProLeuAsnTyrAsnPheTyrArgAlaSerGln 297
XX ||||||| :
XX 857 ATTCTGCTTTGATGTCCTCCCTTCATTATAATCTTTATAACGCGCTCAAT 906
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XX 298 GlnGlyGlySerTyrAspMetArgAsnIleLeuArgGlySerLeuValG 314
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XX 907 AGTGGAGCAACTATGATCGCAAACTTCTTAATGAACGGTGTGTCA 956
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XX 314 uAlaHisPromethisAlaValThrPheValAspAsnHisAspThrGlnp 331
XX : ||||||| :
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XX ||||||| :
XX 331 roGlyGlySerLeuGluSerTyrPheValAlaAspTrpPheLysProLeuAla 347
XX ||||||| :
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XX 348 TyrAlaThrIleLeuThrArgGlyGlyTyrProAsnValPheTyrG 364
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XX 1057 TATCGGCTTATTTAAACAAGAGAACAAGGCTATCCCTGCTGCTTCTATGG 1106
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XX 364 yAspTyrTyrGlyIleProAsnAspAsnIleSerAlaLysLysAspMetI 381
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XX 1107 TGACTACTGGAATTCACACATAGTGTCCACGCAATGAAGCCCAAGA 1156
XX ||||||| :
XX 381 leAspGluLeuLeuAspAlaArgGlnAsnTyrAlaTyrGlyThrGlnHis 397
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XX 1157 TTGATCCAATCTTAGAGCGCGCTCAAAATTTTGCATATGGAACAACAAT 1206
XX ||||||| :
XX 398 AspTyrPheAspHisTyrAspValValGlyTyrPheArgGluGlySerSe 414
XX ||||||| :
XX 1207 GATATTTTACCACATCATATATATATCGGATGGACACGTGAAGGAATAC 1256
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XX 1257 CACGCATCCCAATTCAGGACTTGGACTATCATGTCGGATGGCGCAGGG 1306
XX ||||||| :
XX 431 lySerLysTrpMetTyrValGlyArgGlnAsnAlaGlyGlnThrTrpThr 447
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XX 448 AspLeuThrGlyAsnAsnGlyAlaSerValThrIleAsnGlyAspGlyTr 464
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XX 1357 GACATACTGGAATAAACCAGGACAGTACGATCAATCGATGGATG 1406
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XX 464 pGlyGluPhePheThrAsnGlyGlySerValSerValTyrValAsnGln 480
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XX 1407 GGCTAATTTTCAGTAATGAGGATCTGTTCCATTTGGGTGAAACGA 1455
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seq_name: /SDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:AAx57593

seq_documentation_block:
ID AAX57593 standard; DNA; 1455 BP.
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AC AAX57593;
XX
DT 16-JUL-1999 (first entry)
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DE Wild type Termamyl(RTM)-like alpha-amylase coding sequence #2.
XX
KW Variant; Termamyl; alpha-amylase; mutation; Bacillus; detergent;
KW dishwashing; laundry; textile; desizing; starch liquefaction;
KW sweetener; ethanol; ss.
XX
OS Bacillus sp.
XX

PN W09919467-Al.
XX
PD 22-APR-1999.
XX
PF 13-OCT-1998; 98WO-DK00444.
XX
PR 13-OCT-1997; 97DK-0001172.
XX
PA (NOVO) NOVO-NORDISK AS.
XX
PI Bisgard-Frantzen H, Borchert TV, Svendsen A;
XX
DR WPI; 1999-277632/23.
XX
PT Variant alpha-amylases - useful as detergents or for textile
XX desizing or starch liquefaction
XX
PS Disclosure; Page 77-78; 93pp; English.
XX
CC This sequence represents the coding sequence for a parent sequence
CC used to generate new variants of a Termamyl-like alpha-amylase with
CC alpha-amylase activity. The variants comprise mutations in 2-6
CC regions/positions relative to an alpha-amylase from either of two
CC Bacillus species in W09526397, B. stearothermophilus, B. licheniformis,
CC B. amyloliquefaciens or Bacillus sp. #707. The alpha-amylase variants
CC are detergent additives for use in detergents for dishwashing, manual
CC or automatic laundry. The variants can also be used for textile desizing
CC or starch liquefaction (e.g. for production of sweeteners or ethanol).
XX
SQ Sequence 1455 BP; 473 A; 227 C; 352 G; 403 T; 0 other;

alignment_scores:
Quality: 1860.50 Length: 483
Ratio: 4.327 Gaps: 2
Percent Similarity: 89.027 Percent Identity: 66.460
alignment_block:
US-09-590-375-1 x AAX57593 ..
Align seg 1/1 to: AAX57593 from: 1 to: 1455

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17 nAspGlyGlnHisTyrAsnArgLeuHisAspAspAlaAlaLeuSerA 34
||| ||||||| :
57 TGATGGGAATCACTGGAATAGATTAGAGATGATCTAGTAACTAAGAA 106
||| ||||||| :
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: : ||||||| :
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||| ||||||| :
51 GlnAlaAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuGlyGluPh 67
||| ||||||| :
157 CAAATGATGTGGGGTATGGAGCTATGATCTTTATGATTTAGGGAAT 206
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67 eAsnGlnLysGlyThrValArgThrLysTyrGlyThrLysAlaGlnLeuG 84
||| ||||||| :
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84 luArgAlaIleGlySerLeuLysSerAsnAspIleAsnValTyrGlyAsp 100
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257 AGTCTGCCATCCATGCTTTAAAGAATAATGGCGTTCAAGTTTATGGGAT 306
||| ||||||| :
101 ValValMetAsnHisLysMetGlyAlaAspPheThrGluAlaValGlnAl 117
||| ||||||| :
307 GTAGTGATGAACCATAAAGGAGGAGCTGATGCTACAGAAACGCTTCTTC 356
||| ||||||| :
117 aValGlnValAsnProThrAsnArgTrpGlnAspIleSerGlyAlaTyr 134
||| ||||||| :
357 GTCTGAGGTGAATCCAAATAACCGGAATCAAGAAATATCTGGGCACTACA 406
||| ||||||| :
XX

134 hrIleAspAlaTrpThrGlyPheAspPheSerGlyArgAsnAlaTyr 150
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
407 CAATTGAGGCTTGGACTAAGTTTGGATTTTCCAGGGGAGGTAATACATAC 456

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167 nArgTyTrGln...GluAsnHisIlePheArgPheAlaAsnThrAsn... 181
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182 ..TrpAsnTrpArgValAspGluGluAsnGlyAsnTyTrAspTyTrLeuLeu 197
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264 sAspAspValGlyAlaLeuGluPheTyTrLeuAspGluMetAsnTrpGluM 281
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281 etSerLeuPheAspValProLeuAsnTyTrAsnPheTyTrArgAlaSerGln 297
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331 roGlyGluSerLeuGluSerTrpValAlaAspTrpPheLysProLeuAla 347
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
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431 lySerLysTrpMetTyTrValGlyArgGlnAsnAlaGlyGlnThrTrpThr 447
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seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:AAx57598

seq_documentation_block:

ID: AAx57598 standard; DNA; 1455 BP.

XX AAx57598;

XX DT 16-JUL-1999 (first entry)

XX DE Wild type Termamyl (RTM)-like alpha-amylase coding sequence #7.

XX KW Variant; Termamyl; alpha-amylase; mutation; Bacillus; detergent;

XX KW dishwashing; laundry; textile; desizing; starch liquefaction;

XX KW sweetener; ethanol; ss.

XX OS Bacillus sp.

XX PN W09919467-A1.

XX XX 22-APR-1999.

XX PF 13-OCT-1998; 98WO-DK00444.

XX XX 13-OCT-1997; 97DK-0001172.

XX XX (NOVO) NOVO-NORDISK AS.

XX PI Bisgard-Frantzen H, Borchert TV, Svendsen A;

XX DR WPI; 1999-277632/23.

XX PT Variant alpha-amylases - useful as detergents or for textile

XX desizing or starch liquefaction

XX PS Disclosure; Page 84-85; 93pp; English.

XX CC This sequence represents the coding sequence for a parent sequence
used to generate new variants of a Termamyl-like alpha-amylase with
alpha-amylase activity. The variants comprise mutations in 2-6
regions/positions relative to an alpha-amylase from either of two
Bacillus species in W09526397, B. stearothermophilus, B. licheniformis,
B. amyloliquefaciens or Bacillus sp. #707. The alpha-amylase variants
are detergent additives for use in detergents for dishwashing, manual
or automatic laundry. The variants can also be used for textile desizing
or starch liquefaction (e.g. for production of sweeteners or ethanol).

XX SQ Sequence 1455 BP; 473 A; 227 C; 352 G; 403 T; 0 other;

alignment_scores:

Quality: 1860.50 Length: 483

Ratio: 4.327 Caps: 2

Percent Similarity: 89.027 Percent Identity: 66.460

alignment_block:

US-09-590-375-1 x AAx57598 ..

Align seg 1/1 to: AAx57598 from: 1 to: 1455

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57 TGATGGGAATCACTGGAATAGATTAAAGATGATGCTAGTAATAAGAA 106
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34 spAlaGlyIleThrAlaIleTrpIleProProAlaTrpLysGlyAsnSer 50
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407 CAATTGAGGCTTGACTAAGTTTGTATTTCCAGGAGGGGTAAATACATAC 456
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182 ..TrpAsnTrpArgValAspGluGluAsnGlyAsnTrpAspTrpLeuLeu 197
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557 CATGGGATTGGGAAGTAGATTCCGAAATGGAATATGATTATTAATG 606
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248 GlnArgAsnGluAlaAspGlnAspLeuPheValValGlyGluTrpTrpLy 264
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281 etSerLeuPheAspValProLeuAsnTrpAsnPheTrpArgAlaSerGln 297
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957 AAAGCATCCAATCGATCGCGTACTTTTGGATAATACAGATTCACAC 1006
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
331 roGlyGluSerLeuGluSerTrpValAlaAspTrpPheLysProLeuAla 347
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1007 CTGGGAATCATTAGAAATCAATTTGTACAAGAATGGTTAAAGCCACTTGC 1056
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
348 TyrAlaThrIleLeuThrArgGluGlyGlyTrpProAsnValPheTrpG 364
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1057 TATGCGCTTATTTTAAACAAGAAACAAGGCTATCCCTCTCTCTTATGG 1106
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
364 YAspTrpTrpGlyIleProAsnAspAsnIleSerAlaLysLysAspMet 381
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1107 TGACTACTATGGAATCCCAACACATAGTCCAGCAATGAAGCCCAAGA 1156
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
381 leAspGluLeuLeuAspAlaArgGlnAsnTrpAlaTrpGlyThrGlnHis 397
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1157 TTGATCCAATCTTAGAGCGCGTCAAAATTTTGCATATGGAACACACAT 1206
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
398 AspTrpPheAspHisTrpAspValValGlyTrpThrArgGluGlySerSe 414
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1207 GATATTTTGACCATCATATATATCGGATGACACGTGAAGAAATAC 1256
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
414 rSerArgProAsnSerGlyLeuAlaThrIleMetSerAsnGlyProGlyG 431
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1257 CACGCATCCCAATTCAGGACTTCGCACTCATCTCGGATGGCCAGGG 1306
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
431 lySerLysTrpMetTrpValGlyArgGlnAsnAlaGlyGlnThrTrpThr 447
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1307 GAGAGAAATGGATGTAGTAGGCGCAAAATAAAGCAGGTCAAGTTTGGCAT 1356
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448 AspLeuThrGlyAsnAsnGlyAlaSerValThrIleAsnGlyAspGlyTr 464
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1357 GACATACCTGGAATAAACCCAGGACAGTTTACCATCAATCGCATGGATG 1406
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
464 pGlyGluPhePheThrAsnGlyGlySerValSerValTrpValAsnGln 480
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1407 GCCTAATTTTCAGTAAATGGAGGATCTGTTCCATTTGGGTGAAACGA 1455
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seq_name: /SID52/gcgdata/geneseq/geneseq/NA2000.DAT:AAA48481
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seq_documentation_block:
ID AAA48481 standard; DNA; 1455 BP.
XX
AC AAA48481;
XX
DT 04-SEP-2000 (first entry)
XX
DE Bacillus parent Termamyl-like alpha-amylase DNA sequence #2.
XX
KW Bacillus; alpha-amylase; washing; textile desizing;
KW starch liquefaction; saccharification; mutein; mutant;
KW enzyme stability; hybrid; ss.
XX
OS Bacillus sp.
XX
FH Key Location/Qualifiers
FT CDS 1..1455
FT /tag= a
FT /product= "Termamyl-like alpha-amylase"
FT /partial
XX
PN WO200029560-A1.
XX
PD 25-MAY-2000.
XX
PF 16-NOV-1999; 99WO-DK00628.
PR 16-NOV-1998; 98DK-0001495.
XX
PA (NOVO ) NOVO-NORDISK AS.
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XX Svendsen A, Kjaerulff S, Bisgard-Frantzen H, Andersen C;
XX WPI: 2000-387777/33.
DR P-PSDB; AAY99603.

XX Variant of parent termamyl-like alpha amylase useful for washing,
PT textile desizing and starch liquefaction, comprising alterations in one
PT or more solvent exposed amino acid residues

XX Disclosure; Page 66-67; 80pp; English.

CC The present sequence encodes a parent Termamyl-like alpha-amylase
CC from which mutants with increased stability at acidic pH, low calcium
CC concentration and high temperatures have been derived. The sequence was
CC isolated from a Bacillus genomic DNA library. A variant may contain
CC mutations in one or more solvent exposed amino acid residues to increase
CC the overall hydrophobicity of the enzyme or the overall number of
CC methyl groups in the side chains of exposed residues may be increased.
CC The mutations can be incorporated by site-directed mutagenesis or by
CC random mutagenesis. As a result of their increased stability, the
CC variants are suitable for the industrial processing of starch, i.e.
CC starch liquefaction and saccharification. They may also be useful for
CC washing, dishwashing and textile desizing. Hybrid alpha-amylases
CC comprising partial amino acid sequences derived from two or more
CC alpha-amylases have also been created in order to increase enzyme
CC stability.

XX Sequence 1455 BP; 473 A; 227 C; 352 G; 403 T; 0 other;

alignment_scores:
Quality: 1860.50 Length: 483
Ratio: 4.327 Gaps: 2
Percent Similarity: 89.027 Percent Identity: 66.460

alignment_block:

US-09-590-375-1 x AAA48481 ..

Align seg 1/1 to: AAA48481 from: 1 to: 1455

1 AspGlyLeuAsnGlyThrMetMetGlnTyrTyrGluTyrPheHisLeuGluAs 17
7 AATGGACAAATGGGACGATGATGCAATACTTTGAATGGCACTTGCCCTAA 56
17 nAspGlyGlnHisTrpAsnArgLeuHisAspAspAlaAlaLeuSerA 34
57 TGATGGGAATCACTGGAATAGATTAGAGATGATGCTAGTAATCTAAGAA 106
34 spAlaGlyIleThrAlaIleTrpIleProAlaTyrLySerGlyAsnSer 50
107 ATAGAGGTATAACCGCTATTTCGATTCGCCCTCGCTGAAAGGGACTTCG 156
51 GlnAlaAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuGlyGluPh 67
157 CAAATATGATGGGTATGGGACCTATGATCTTTATGATTTAGGGGAAT 206
67 eAsnGlnLyGlyThrValArgThrLySerGlyThrLyAlaGlnLeuG 84
207 TAATCAAAAGGGGCGGTTCGTACTAAGTATGGGACACGTAGTCAATTGG 256
84 luArgAlaIleGlySerLeuLySerAsnAspIleAsnValTyrGlyAsp 100
257 AGTCCTGCCATCATGCTTTAAAGATAATAGCGCTTCAAGTTTATGGGAT 306
101 ValValMetAsnHisLysMetGlyAlaAspPheThrGluAlaValGlnAl 117
307 GTAGTGATGAACCAATAAGGAGGAGCTGATGCTACAGAAAACGTTCTTC 356
117 aValGlnValAsnProThrAsnArgTrpGlnAspIleSerGlyAlaTyrT 134
357 TGTCAGGTGAATCCAAATACCGGAATCAAGAAATATCTGGGGGACTACA 406

134 hrIleAspAlaTrpThrGlyPheAspPheSerGlyArgAsnAsnAlaTyr 150
407 CAATTGAGGCTTGGACTAGTTTGGATTTCCAGGGAGGGGTAATACATAC 456
151 SerAspPheLysTrpArgTrpPheHisPheAsnGlyValAspTrpAspG 167
457 TCAGACTTTAAATGGCTTGGTATCATTTTCGATGGTGTAGATTGGGATCA 506
167 nArgTyrGln...GluAsnHisIlePheArgPheAlaAsnThrAsn... 181
507 ATCAGACAAATCCAAATCGTATCTACAAATCCGAGGTGATGGTAAGG 556
182 ..TrpAsnTrpArgValAspGluGluAsnGlyAsnTyrAspTyrLeuLeu 197
557 CATGGGATTTGGGAAGTATGATTCGGAAATGGAATATGATATTATTAAG 606
198 GlySerAsnIleAspPheSerHisProGluValGlnAspGluLeuLysAs 214
607 TATGCAGATGTAGATATGATTCGGAGGTAGTAATAGCTTAGAAG 656
214 pTrpGlySerTrpPheThrAspGluLeuAspGlyTyrArgLeuA 231
657 ATGGGGAGNAATGGTATACAAATACATTAATCTTGATGGATTTAGGATCG 706
231 spAlaIleLysHisIleProPheTrpTyrThrSerAspTrpValArgHis 247
707 ATGCGGTGAAGCATATTAATATAGCTTTACACGTGATTGGTTGACCCAT 756
248 GlnArgAsnGluAlaAspGlnAspLeuPheValValGlyGlyTyrTrp 264
757 GTAAGAAACGCAACGGGAAAGAAATGTTGCTGTGCTGAATTTTGGAA 806
264 sAspAspValGlyAlaLeuGluPheTyrLeuAspGluMetAsnTrpGlu 281
807 AATGATTTAGTGCTCTGGAGAACTATTTAAATAAACAACAACTGGAATC 856
281 etSerLeuPheAspValProLeuAsnTyrAsnPheTyrArgAlaSerGln 297
857 ATTCGTCTTTGATGTCCTTCATTAATATCTTTATAACGGCTCAAT 906
298 GlnGlyGlySerTyrAspMetArgAsnIleLeuArgGlySerLeuValG 314
907 AGTGGAGGCAACTATGACATGCGCAAACTCTTAATGGAACGGTTGTCCA 956
314 uAlaHisProMetHisAlaValThrPheValAspAsnHisAspThrGln 331
957 AAAGCATCCATGCATGCCGTAACTTTTGGATATATCAGATTCTCAAC 1006
331 roGlyGluSerLeuGluSerTrpValAlaAspTrpPheLysProLeuAla 347
1007 CTGGGGAATCATAGAAATCATTTGTACAAGAAATGGTTTAAGCCACTTGC 1056
348 TyrAlaThrIleLeuThrArgGluGlyTyrProAsnValPheTyrG 364
1057 TATGGCTTATTTTAAACAAGAGAACAAGGCTATCCCTCTCTCTCTATGG 1106
364 yAspTyrTyrGlyIleProAsnAspAsnIleSerAlaLysLysAspMet 381
1107 TGACTACTATGGAATTCACACATAGTGTCCAGCAATGAAAGCCCAAGA 1156
381 leAspGluLeuLeuAspAlaArgGlnAsnTyrAlaTyrGlyThrGlnHis 397
1157 TTGATCCAATCTTAGAGGGCGCTCAAAATTTTGCATATGGAACACACAT 1206
398 AspTyrPheAspHisTrpAspValValGlyTyrTrpThrArgGluGlySer 414
1207 GATTATTTTGACCATCAATAATAATCGGATGGACACGTCGAAAGGAATAC 1256
414 rSerArgProAsnSerGlyLeuAlaThrIleMetSerAsnGlyProGlyG 431
1257 CACGATCCCAATTCAGGACTTGCAGACTATCATGTGGATGGGCCAGGGG 1306
431 lySerLysTrpMetTyrValGlyArgGlnAsnAlaGlyGlnThrTrpThr 447

1307 GAGAGAAATGGATGATACAGGCAAAATAAAGCAGGTCAAGTTTGGCAT 1356
448 AspLeuThrGlyAsnAsnGlyAlaSerValThrIleAsnGlyAspGlyTr 464
1357 GACATAACTGGAATAAACACAGGACAGTTACGATCAATGCAGATGGATG 1406
464 pGlyGluPhePheThrAsnGlyGlySerValSerValThrValAsnGln 480
1407 GGCTAAATTTTCAGTAAATGAGGAGCTGTTCCATTGGGTGAAACGA 1455

seq_name: /SIDS2/gcgdata/geneseq/geneseq/NA2000.DAT.AAA48486

seq_documentation_block:

ID AAA48486 standard; DNA; 1455 BP.

XX AAA48486;

XX 04-SEP-2000 (first entry)

XX Bacillus Termamyl-like alpha-amylase DNA sequence #4.

XX Bacillus; alpha-amylase; washing; textile desizing;
KW starch liquefaction; saccharification; muten; mutant;
XX enzyme stability; hybrid; ss.

XX Bacillus sp.

XX Key Location/Qualifiers
FH 1..1455
CDS

FT *tag= a
FT /product= "Termamyl-like alpha-amylase"
FT /partial

XX WO200029560-A1.

XX 25-MAY-2000.

XX 16-NOV-1999; 99WO-DK00628.

XX 16-NOV-1998; 98DK-0001495.

XX (NOVO) NOVO-NORDISK AS.

XX Svendsen A, Kjaerulff S, Bisgard-Frantzen H, Andersen C;

XX WPI; 2000-38777/33.

XX P-PSDB; AAY99609.

XX Variant of parent termamyl-like alpha amylase useful for washing,
PT textile desizing and starch liquefaction, comprising alterations in one
PT or more solvent exposed amino acid residues

XX Disclosure; Page 70-71; 80pp; English.

XX The present sequence encodes a parent alpha-amylase from which mutants
CC with increased stability at acidic pH, low calcium concentration and high
CC temperatures have been derived. The sequence was isolated from a Bacillus
CC genomic DNA library. A variant may contain mutations in one or more
CC solvent exposed amino acid residues to increase the overall
CC hydrophobicity of the enzyme or the overall number of methyl groups in
CC the side chains of exposed residues may be increased. The mutations can
CC be incorporated by site-directed mutagenesis or by random mutagenesis. As
CC a result of their increased stability, the variants are suitable for the
CC industrial processing of starch, i.e. starch liquefaction and
CC saccharification. They may also be useful for washing, dishwashing and
CC textile desizing. Hybrid alpha-amylases comprising partial amino acid
CC sequences derived from two or more alpha-amylases have also been created
CC in order to increase enzyme stability.

XX Sequence 1455 BP; 473 A; 227 C; 352 G; 403 T; 0 other;

alignment_scores:

Quality: 1860.50 Length: 483
Ratio: 4.327 Gaps: 2
Percent Similarity: 89.027 Percent Identity: 66.460

alignment_block:

US-09-590-375-1 x AAA48486 ..

Align seg 1/1 to: AAA48486 from: 1 to: 1455

1 AspGlyLeuAsnGlyThrMetMetGlnTyrTyrGluTrpHisLeuGluAs 17
7 AATGGGCAAAATGGGAGCATGATGCAATACTTTGAATGGCACTTGCCTAA 56
17 nAspGlyGlnHisTrpAsnArgLeuHisAspAspAlaAlaAlaLeuSerA 34
57 TGATGGGAATCACTGGATAGATAGATAGATAGATAGATAGATAGATAGAA 106
34 spAlaGlyIleThrAlaIleTrpIleProAlaTyrLysGlyAsnSer 50
107 ATAGAGGTATACCGCTATTTGGATTCGCTCGCTGGAAAGGACTTCG 156
51 GlnAlaAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuGlyGluPh 67
157 CAAAATGATGTGGGTATGGAGCTATGATCTTTATGATTTAGGGGAAT 206
67 eAsnGlnLysGlyThrValArgThrLysTyrGlyThrLysAlaGlnLeuG 84
207 TAATCAAAAGGGGACGGTTCGTACTAAGTATGGACACGTAGTCAATGG 256
84 luArgAlaIleGlySerLeuLysSerAsnAspIleAsnValTyrGlyAsp 100
257 AGTCTGCCATCCATGCTTTAAAGAATAATGGCGTTCAAAGTTTATGGGAT 306
101 ValValMetAsnHisLysMetGlyAlaAspPheThrGluAlaValGlnAl 117
307 GTAGTGTGAACCATTAAGAGGAGGCTGATGCTACAGAAACGTTCTTTC 356
117 aValGlnValAsnProThrAsnArgTrpGlnAspIleSerGlyAlaTyrT 134
357 TGTCGAGGTGAATCCAAATAACCGGAATCAAGAAATATCTGGGGACTACA 406
134 hrIleAspAlaTrpThrGlyPheAspPheSerGlyArgAsnAlaTyr 150
407 CAATTGAGGCTTGGAATAAGTTTGATTTCCAGGAGGGGTATACATAC 456
151 SerAspPheLysTrpArgTrpPheHisPheAsnGlyValAspTrpAspG 167
457 TCAGACTTAAATGGGCTGGTATCATTTCCGATGGTGTAGATGGGATCA 506
167 nArgTyrGln...GluAsnHisIlePheArgPheAlaAsnThrAsn... 181
507 ATCAGCACAATTCCAAATCGTATCTACAAATTCGAGGATGGGTAAAGS 556
182 ..TrpAsnTrpArgValAspGluGluAsnGlyAsnTyrAspTrpLeuLeu 197
557 CATGGGATTTGGGAAGTAGATTCGGAATAATGGAATTTATGATTTAATG 606
198 GlySerAsnIleAspPheSerHisProGluValGlnAspGluLeuLysAs 214
607 TATGCAGATGATAGATGATGATCATCCGGAGGTAGTAAATGACGCTTAAAG 656
214 pTrpGlySerTrpPheThrAspGluLeuAspLeuAspGlyTyrArgLeuA 231
657 ATGGGAGAATGGTATACAAATACATAAATCTTGATGGATTTAGGATCG 706
231 spAlaIleLysHisIleProPheTrpTyrThrSerAspTrpValArgHis 247
707 ATGCGGTGAAGCATATTAATATAGCTTTACACGTGATTTGGTTGACCAT 756
248 GlnArgAsnGluAlaAspGlnAspLeuPheValValGlyGlyTyrTrp 264
757 GTAAGAACAACGCAACGGGAAAGAAATGTTTCTGCTGCTGATTTGGAA 806

xx Claim 8; Page 23-26; 40pp: English.
 xx This sequence represents the coding sequence for an alkaline liquefying
 CC alpha-amylase. Alpha-amylase is an enzyme that acts on starch-related
 CC polysaccharides, hydrolyzing the alpha-1,4-glucoside bond of the
 CC polysaccharide molecule. Alkaline liquefying alpha-amylases exhibit
 CC resistance to surfactants used in detergents, and decompose starch or
 CC starch-related polysaccharides in a highly random manner. The Bacillus
 CC species KSM-API378, from which this sequence was isolated, is an
 CC alkalophilic Bacillus strain. It was isolated from soil in the vicinity
 CC of the city of Tohchi. The enzyme is useful in improving the efficiency
 CC of dish-washing and laundry detergents, particularly on starch dirt.
 xx
 SQ Sequence 1776 BP; 575 A; 305 C; 417 G; 479 T; 0 other;

alignment_scores:
 Quality: 1853.50 Length: 483
 Ratio: 4.300 Gaps: 2
 Percent Similarity: 89.234 Percent Identity: 66.874

alignment_block:
 US-09-590-375-1 x AAT51339 ..

Align seg 1/1 to: AAT51339 from: 1 to: 1776

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1 AspGlyLeuAsnGlyThrMetMetGlnTyrGluTyrPheHisLeuGluAs 17
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17 nAspGlyGlnHisTrpAsnArgLeuHisAspAlaAlaLeuSera 34
: : : : : | | | | | | | | | | | | | | | | | | | | | | | |
294 TGCGGGAACCACTGGACAGTTACGAGATGACGACCTAACTTAAGA 343

34 spAlaGlyIleThrAlaIleTrpLeuProAlaTyrLysGlyAsnSer 50
: : : : : | | | | | | | | | | | | | | | | | | | | | | | |
344 GTAAGGGATTACCGCTGTTTGGATTCCTCTGATGGAAGGGACCTCG 393

51 GlnAlaAspValGlyTyrGlyValTyrAspLeuTyrAspLeuGlyGluPh 67
: : : : : | | | | | | | | | | | | | | | | | | | | | | | |
394 CAATATGATGTTGGGTATGTTGCTATGATTTGTACGATTTGGTGATT 443

67 eAsnGlnLysGlyThrValArgThrLysTyrGlyThrLysAlaGlnLeu 84
: : : : : | | | | | | | | | | | | | | | | | | | | | | | |
444 TAACCAAAAGGGAACCGCTCCATCAAAATATGGCACAAGGAGTCAGTTGC 493

84 LuArgAlaIleGlySerLeuLysSerAsnAspIleAsnValTyrGlyAsp 100
: : : : : | | | | | | | | | | | | | | | | | | | | | | | |
494 AAGGTGCGGTGACATCTTTGAAAAATAACGGGATTCAGTTTATGGGGAT 543

101 ValValMetAsnHisLysMetGlyValAspPheThrGluAlaValGlnAl 117
: : : : : | | | | | | | | | | | | | | | | | | | | | | | |
544 GTCGTGATGAATCAATAAGGTGGACGACGCGGACAGAGATGGTAATGCG 593

117 aValGlnValAsnProThrAsnArgTrpGlnAspIleSerGlyAlaTyr 134
: : : : : | | | | | | | | | | | | | | | | | | | | | | | |
594 GGTGGAAGTGAACCGAACCAACCGAAACCAAGAAATATCAGGTGAATACA 643

134 hrIleAspAlaTrpThrGlyPheAspPheSerGlyArgAsnAlaTyr 150
: : : : : | | | | | | | | | | | | | | | | | | | | | | | |
644 CCATTTGAAGCATGACGCAAAATTTGATTTCCCTGGAAGAGGAAATACCCAT 693

151 SerAspPheLysTrpArgTrpPheHisPheAsnGlyValAspTrpAspG1 167
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694 TCCAACTTTAAATGGCGTGTATCATATTTGATGGGACAGATTTGGGATCA 743

167 n...ArgTyrGlnGluAsnHisIlePheArgPheAlaAsnThrAsn... 181
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744 GTCAGCTCAGCTTCAGAACCAAAATATATAAATTCAGAGGTACCGGAAGG 793

182 ..TrpAsnTrpArgValAspGluAsnGlyAsnTyrAspTyrLeuLeu 197
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794 CATGGGACTGGGAAGTAGATATAGAGAAACGGCACTATGATTACCTTATG 843
198 GlySerAsnIleAspPheSerHisProGluValGlnAspGluLeuLysAs 214
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844 TATGGCAGACATGATGATGATCATCCAGAGTAATCAATGAACCTTAGAAA 893
214 pTrpGlySerTrpPheThrAspGluLeuAspLeuAspGlyTyrArgLeuA 231
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894 TTGGGAGCTTTGGTATACAAATACACTTAATCTAGATGGATTTAGAATCG 943
231 spAlaIleLysHisIleProPheTrpTyrThrSerAspTrpValArgHis 247
: : : : : | | | | | | | | | | | | | | | | | | | | | | | |
944 ATGCTGTGAACATATTAATATACAGCTATACAGAGATTTGGCTAACACAT 993
248 GlnArgAsnGluAlaAspGlnAspLeuPheValValGlyGluTyrTrp 264
: : : : : | | | | | | | | | | | | | | | | | | | | | | | |
994 GTGCGTAACACCACAGGTAAACCAATGTTGCGAGTTGCAGAAATTTGGNA 1043
264 sAspAspValGlyAlaLeuGluPheTyrLeuAspGluMetAsnTrpGluM 281
: : : : : | | | | | | | | | | | | | | | | | | | | | | | |
1044 AATGACCTTGTGCTCAATCGAAACATATTTAAATAAAACAAGTTGGAATC 1093
281 etSerLeuPheAspValProLeuAsnTyrAsnPheTyrArgAlaSerGln 297
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1094 ACTCGGTGTCGATGTTCTCTTCAATTAATTTGTACAATGCATCTAAT 1143
298 GlnGlyGlySerTyrAspMetArgAsnIleLeuArgGlySerLeuValG1 314
: : : : : | | | | | | | | | | | | | | | | | | | | | | | |
1144 AGTGTGGCTATTTGATATGAGAAATATTTAAATGTTCTGTCTGTACA 1193
314 uAlaHisProMetHisAlaValThrPheValAspAsnHisAspThrGlnP 331
: : : : : | | | | | | | | | | | | | | | | | | | | | | | |
1194 AAACACCCCTATACATGCAGTCACATTTTGTGATAACCATGACTCTCAGC 1243
331 roGlyGluSerLeuGluSerTrpValAlaAspTrpPheLysProLeuAla 347
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348 TyrAlaThrIleLeuThrArgGlyGlyTyrProAsnValPheTyrG1 364
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398 AspTyrPheAspHisTrpAspValValGlyTyrTrpThrArgGlySerSe 414
: : : : : | | | | | | | | | | | | | | | | | | | | | | | |
1444 GATTATTTTGTATCATCATGATATTTATCGCTGGCAGCAGAGAGGGACAG 1493
414 rSerArgProAsnSerGlyLeuAlaThrIleMetSerAsnGlyProGlyG 431
: : : : : | | | | | | | | | | | | | | | | | | | | | | | |
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431 lySerLysTrpMetTyrValGlyArgGlnAsnAlaGlyGlnThrTrpThr 447
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1544 GTAATAAATGGATGATGTCGGGAAACATAAAGCTGGCCAAAGTATGGAGA 1593
448 AspLeuThrGlyAsnAsnGlyAlaSerValThrIleAsnGlyAspGlyTr 464
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1594 GATATCACCAGGAATAGGTCTGTACCGCTCACCATTAAATGACAGATGGT 1643
464 pGlyGluPhePheThrAsnGlyGlySerValSerValTyrValAsnGln 480
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seq_documentation_block:

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ID AAC66234 standard; DNA; 1786 BP.

XX AAC66234;

XX
DT 19-FEB-2001 (first entry)

XX
DE Mutant alpha-amylase nucleotide sequence.

XX
KW Alpha-amylase; detergent; Bacillus; ds.

XX Bacillus sp.

XX
PN JP2000245466-A.

XX
PD 12-SEP-2000.

XX
PF 25-FEB-1999; 99JP-0048213.

XX
PR 25-FEB-1999; 99JP-0048213.

XX
PA (KAOS) KAO CORP.

XX
DR WPI; 2000-615143/59.

DR P-PSDB; AAB35714.
XX

PT A novel mutant alpha-amylase for use in a detergent composition -

XX
PS Example 1; Page 6-9; 12pp; Japanese.

XX
CC The present invention relates to a mutant alpha-amylase. Included in the
CC invention are a gene encoding the mutant alpha-amylase, a vector
CC containing the gene, and a transformed cell recombinant by the vector. The
CC enzyme is used in a detergent composition. The present sequence
CC represents the mutant alpha-amylase gene.

Sequence 1786 BP; 578 A; 307 C; 420 G; 481 T; 0 other;

alignment_scores:

Quality:	1853.50	Length:	483
----------	---------	---------	-----

Ratio: 4.300
Gaps: 2

Percent Similarity: 89.234 Percent Identity: 66.874

alignment_block:

US-09-590-375-1 X AAC66234

Align seg 1/1 to: AAC66234 from: 1 to: 1786

1 AspGlyLeuAsnGlyThrMetMetGlnTyrTyrGluTrpHisLeuGluAs 17

254 AATGGGACGAATGGGACCATGATGCAGTATTTTGAATGGCATTGCCAAA 303

17 nAspGlyGlnHisTrpAsnArgLeuHisAspAspAlaAlaLeuSera 34

304 TGACGGGAACCACTGGAACAGGTTACGAGATGACGCAGCTAACTTAAAGA 353

34 spAlaGlyIleThrAlaIleTrpIleProProAlaTyrLysGlyAsnSer 50

354 GTAAAGGGATTACCGCTGTTTGGATTCCCTCGCATGGAAAGGGACTTCG 403

51 GlnAlaAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuGlyGluph 67

404 CAAATGATGTTGGGTATGGTGCCTATGATTGTACGATCTTGCTGAGTT 453

67 eAsnGlnLysGlyThrValArgThrLysTyrGlyThrLysAlaGlnLeuG 84

454 TAACCAAAGGGAACCGTCCGTACAAAATATGGCACAAGGAGTCAGTTGC 503

84 luArgAlaIleGlySerLeuLysSerAsnAspIleAsnValTyrGlyAsp 100

504 AAGGTCCCGTGACATCTTTGAAAAATAACGGGATTCAAGTTTATGGGGAT 553

101 valValMetAsnHisLysMetGlyAlaAspPheThrGluAlaValGlnAl 117

[illegible]

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 28, 2001, 16:54:37 ; Search time 33.83 Seconds
(without alignments)
1050.996 Million cell updates/sec

Title: US-09-590-375-1
Perfect score: 2687
Sequence: 1 DGLNGTMQYVHLENDGQ.....GDGWGEFTNGGVSIVVQ 480

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_1101.*
1: /SIDS2/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SIDS2/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SIDS2/gcgdata/geneseq/geneseq/AA1982.DAT.*
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6: /SIDS2/gcgdata/geneseq/geneseq/AA1985.DAT.*
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16: /SIDS2/gcgdata/geneseq/geneseq/AA1995.DAT.*
17: /SIDS2/gcgdata/geneseq/geneseq/AA1996.DAT.*
18: /SIDS2/gcgdata/geneseq/geneseq/AA1997.DAT.*
19: /SIDS2/gcgdata/geneseq/geneseq/AA1998.DAT.*
20: /SIDS2/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SIDS2/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SIDS2/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2687	100.0	501	21 AAB14822	Bacillus sp. lique
2	2618	97.4	501	21 AAB14821	Bacillus sp. lique
3	1920.5	71.5	483	21 AAB29340	Bacillus sp. matur
4	1919.5	71.4	483	21 AAB29318	Bacillus sp. matur
5	1915.5	71.3	483	21 AAB29342	Bacillus sp. matur
6	1915.5	71.3	483	21 AAB29343	Bacillus sp. matur
7	1915.5	71.3	483	21 AAB29372	Bacillus sp. matur
8	1914.5	71.3	483	21 AAB29325	Bacillus sp. matur
9	1914.5	71.3	483	21 AAB29341	Bacillus sp. matur
10	1913.5	71.2	483	21 AAB29345	Bacillus sp. matur
11	1913.5	71.2	483	21 AAB29346	Bacillus sp. matur

12	1913.5	71.2	483	21 AAB29348	Bacillus sp. matur
13	1913.5	71.2	483	21 AAB29349	Bacillus sp. matur
14	1913.5	71.2	483	21 AAB29351	Bacillus sp. matur
15	1913.5	71.2	483	21 AAB29352	Bacillus sp. matur
16	1912.5	71.2	483	21 AAB29338	Bacillus sp. matur
17	1912.5	71.2	483	21 AAB29339	Bacillus sp. matur
18	1912.5	71.2	483	21 AAB29344	Bacillus sp. matur
19	1912.5	71.2	483	21 AAB29347	Bacillus sp. matur
20	1912.5	71.2	483	21 AAB29350	Bacillus sp. matur
21	1911.5	71.1	483	21 AAB29337	Bacillus sp. matur
22	1911.5	71.1	483	21 AAB29336	Bacillus sp. matur
23	1910.5	71.1	483	21 AAB29321	Bacillus sp. alpha
24	1910.5	71.1	483	21 AAB29374	Bacillus sp. matur
25	1910.5	71.1	483	21 AAB29375	Bacillus sp. matur
26	1910.5	71.1	483	21 AAB29310	Bacillus sp. matur
27	1909.5	71.1	483	21 AAB29322	Bacillus sp. alpha
28	1909.5	71.1	483	21 AAB29373	Bacillus sp. matur
29	1908.5	71.0	483	21 AAB29377	Bacillus sp. matur
30	1908.5	71.0	483	21 AAB29378	Bacillus sp. matur
31	1908.5	71.0	483	21 AAB29380	Bacillus sp. matur
32	1908.5	71.0	483	21 AAB29381	Bacillus sp. matur
33	1908.5	71.0	483	21 AAB29383	Bacillus sp. matur
34	1908.5	71.0	483	21 AAB29384	Bacillus sp. matur
35	1907.5	71.0	483	21 AAB29370	Bacillus sp. matur
36	1907.5	71.0	483	21 AAB29371	Bacillus sp. matur
37	1907.5	71.0	483	21 AAB29376	Bacillus sp. matur
38	1907.5	71.0	483	21 AAB29379	Bacillus sp. matur
39	1907.5	71.0	483	21 AAB29382	Bacillus sp. matur
40	1906.5	71.0	483	21 AAB29323	Bacillus alpha-amy
41	1906.5	71.0	483	21 AAB29369	Bacillus sp. matur
42	1906.5	71.0	485	21 AAB29332	Bacillus sp. matur
43	1906.5	71.0	485	21 AAB29368	Bacillus sp. matur
44	1905.5	70.9	483	21 AAB29328	Bacillus sp. alpha
45	1905.5	70.9	485	21 AAB29311	Bacillus sp. matur

ALIGNMENTS

RESULT 1
AAB14822
ID AAB14822 standard; protein: 501 AA.
XX
AC AAB14822;
XX
DT 19-DEC-2000 (first entry)
XX
DE Bacillus sp. liquefying alpha-amylase #2.
XX
KW Liquefying alpha-amylase; detergent; starch industry; brewing industry;
KW pharmaceutical industry; food industry; fibre industry.
XX
OS Bacillus sp.
XX
PN EPI022334-A2.
XX
PD 26-JUL-2000.
XX
PF 20-DEC-1999; 99EP-0125399.
XX
PR 21-DEC-1998; 98JP-0362487.
PR 21-DEC-1998; 98JP-0362488.
XX
(KAOS) KAO CORP.
XX
Hagiwara H, Kitayama K, Hayashi Y, Igarashi K, Endo K, Ozaki K;
WPI: 2000-516014/47.
N-PSDB: AAA70314.

PT New liquefying alkaline amylase, useful in a detergent composition
comprises a residual activity of not less than 70 % when treated under
specific conditions -

```

XX PS Claim 4; Page 17-19; 34pp; English.
XX PA
XX CC The present sequence is a novel alpha-amylase from Bacillus sp. The
XX CC invention concerns the isolation of two new liquefying alpha-amylases
XX CC from Bacillus sp. strains KSM-K36 and KSM-K38, designated K36 and K38, of
XX CC which this protein is one. The present alpha-amylases are chelating-agent
XX CC resistant and thus are useful in the starch, brewing, fibre,
XX CC pharmaceutical and food industries, and especially as components of
XX CC detergents.
XX SQ Sequence 501 AA;

Query Match 100.0%; Score 2687; DB 21; Length 501;
Best Local Similarity 100.0%; Pred. No. 6.6e-214;
Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DGLNGTMMQYYEWHLENDGQHNRLHDDAAALSDAGITAIWIPPAYKGNQADVGAYD 60
DB 22 dglngtmmqyyewhlendgqhnrlhddaaalsdagitaiwippaykgnsqadvgygayd 81
QY 61 LYDLGEFNQKGTVRTKYGTAKLERAIGSLKSNIDINVYGDVVMNHKMGADFTFAVOAVOV 120
DB 82 lydlgefngkgtvrtkygtakleraigslksndinvygdvvmnhkmgadfteavqavqv 141
QY 121 NPTNRWQDISGAYTIDAWTGFSGRNNAYSDFKRWFFHNGVDWDQRYOENHIFRFANT 180
DB 142 nptnrwqdisgaytidawtgdsgnnaysdfkwrwfhngvwdwqryqenhihfrant 201
QY 181 NNNWRVDEENGNYDYLGSNIDFSHPVQDELKMGSWFTDELDDGYRLDAIKHIPFWY 240
DB 202 nnnwrvdeengnydyllgsnidfshpveqdelkdwgsfwtdeldlgyrldaikhpfwy 261
QY 241 TSDWVRHORNEADODLFVVGKDDVGALFYLDEMNMWMSLFDVPLNRYFASQOQG 300
DB 262 tsdwrhrneadodlfvvgkddvgalefylednmwmslfdvplnryfyrasqqgg 321
QY 301 SYDMRNILRGLSVEAHPHMAVTFVDNHDTPQGESLESWADWFKPLAYATILTRGGYPN 360
DB 322 sydmrnilrgslveahphmavtfvndhdtqpgesleswadvwfkplayatiltreggypn 381
QY 361 VFYGDYIGIPNDNISAKKMDIDELLDARQNYAGTQHDYFDHWDVVGWTRGSSSRPNSG 420
DB 382 vfygdyigipndnisakkmdidelldarqnyagtqhdyfhdwvvgwtrgsssrpns 441
QY 421 LATIMNSGPGSKWMYVGRQNGQWTDLTGNNGASVTINGDGWGEFFTNGGSVSVYVNO 480
DB 442 latimngpggskwmvygrnagqwtldtgnngasvtindgwggefftcnggsvsvyvnq 501

RESULT 2
AAB14821
ID AAB14821 standard; protein; 501 AA.
XX AC
XX AC AAB14821;
XX CC
XX CC 19-DEC-2000 (first entry)
XX DT
XX DE Bacillus sp. liquefying alpha-amylase #1.
XX DE Liquefying alpha-amylase; detergent; starch industry; brewing industry;
XX KW pharmaceutical industry; food industry; fibre industry.
XX KW
XX OS Bacillus sp.
XX PN EP1022334-A2.
XX PD
XX PD 26-JUL-2000.
XX PF
XX PF 20-DEC-1999; 99EP-0125399.
XX PF
XX PF 21-DEC-1998; 98JP-0362487.

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PR 21-DEC-1998; 98JP-0362488.
XX PA
XX PA (KAOS ) KAO CORP.
XX PI Hagihara H, Kitayama K, Hayashi Y, Igarashi K, Endo K, Ozaki K;
XX WPI; 2000-516014/47.
XX DR N-PSDB; AAA70313.
XX PT
XX PT New liquefying alkaline amylase, useful in a detergent composition
XX PT comprises a residual activity of not less than 70 % when treated under
XX PT specific conditions
XX PS Claim 4; Page 14-16; 34pp; English.
XX CC The present sequence is a novel alpha-amylase from Bacillus sp. The
XX CC invention concerns the isolation of two new liquefying alpha-amylases
XX CC from Bacillus sp. strains KSM-K36 and KSM-K38, designated K36 and K38, of
XX CC which this protein is one. The present alpha-amylases are chelating-agent
XX CC resistant and thus are useful in the starch, brewing, fibre,
XX CC pharmaceutical and food industries, and especially as components of
XX CC detergents.
XX SQ Sequence 501 AA;

Query Match 97.4%; Score 2618; DB 21; Length 501;
Best Local Similarity 96.5%; Pred. No. 3.3e-208;
Matches 463; Conservative 13; Mismatches 4; Indels 0; Gaps 0;

QY 1 DGLNGTMMQYYEWHLENDGQHNRLHDDAAALSDAGITAIWIPPAYKGNQADVGAYD 60
DB 22 dglngtmmqyyewhlendgqhnrlhddaaalsdagitaiwippaykgnsqadvgygayd 81
QY 61 LYDLGEFNQKGTVRTKYGTAKLERAIGSLKSNIDINVYGDVVMNHKMGADFTFAVOAVOV 120
DB 82 lydlgefngkgtvrtkygtakleraigslksndinvygdvvmnhkmgadfteavqavqv 141
QY 121 NPTNRWQDISGAYTIDAWTGFSGRNNAYSDFKRWFFHNGVDWDQRYOENHIFRFANT 180
DB 142 npsnrwqdisgaytidawtgdsgnnaysdfkwrwfhngvwdwqryqenhihfrant 201
QY 181 NNNWRVDEENGNYDYLGSNIDFSHPVQDELKMGSWFTDELDDGYRLDAIKHIPFWY 240
DB 202 nnnwrvdeengnydyllgsnidfshpveqdelkdwgsfwtdeldlgyrldaikhpfwy 261
QY 241 TSDWVRHORNEADODLFVVGKDDVGALFYLDEMNMWMSLFDVPLNRYFASQOQG 300
DB 262 tsdwrhrneadodlfvvgkddvgalefylednmwmslfdvplnryfyrasqqgg 321
QY 301 SYDMRNILRGLSVEAHPHMAVTFVDNHDTPQGESLESWADWFKPLAYATILTRGGYPN 360
DB 322 sydmrnilrgslveahphmavtfvndhdtqpgesleswadvwfkplayatiltreggypn 381
QY 361 VFYGDYIGIPNDNISAKKMDIDELLDARQNYAGTQHDYFDHWDVVGWTRGSSSRPNSG 420
DB 382 vfygdyigipndnisakkmdidelldarqnyagtqhdyfhdwdivgwtregtsrpsug 441
QY 421 LATIMNSGPGSKWMYVGRQNGQWTDLTGNNGASVTINGDGWGEFFTNGGSVSVYVNO 480
DB 442 latimngpggskwmvygrnagqwtldtgnngasvtindgwggefftcnggsvsvyvnq 501

RESULT 3
AAB29340
ID AAB29340 standard; Protein; 483 AA.
XX AC
XX AC AAB29340;
XX CC
XX CC 09-FEB-2001 (first entry)
XX DT
XX DE Bacillus sp. mature alpha-amylase SEQ ID NO:2 mutant #10.
XX PF
XX PF

```


Matches 333; Conservative 62; Mismatches 85; Indels 1; Gaps 1;

Qy 1 DGLNGTMOYVEWHLNDGQHNRLLHDDAAALSDAGITAIWIPPAYKGNQADVCYGYVD 60
 Db 3 dgtngtimgyfewvnpdgqhnrlhnaqnlknagitaipppawkgtsqndvgygyayd 62

Qy 61 LYDLGEFNQKGTVRTKYGTKAQLERAIGLSKNSDINIVYGDVVMNHKMGADFTFAVOAV 120
 Db 63 lydlgefngkgtvrtkgtkaelerairslkanglqvgydvvmnhkggadfterqvavev 122

Qy 121 NPTNRWQDISGAYTIDAWTGFDFSGRNAYSDFKRWRFHFGVWDQ-RYQENHIFRAN 179
 Db 123 npqnrngvsgtyeavtgnfpgngqhsfkwrwyhfdgtdwdqgrqlsnriykfrg 182

Qy 180 TNWNRVDEENGNDYLLGSNIDFSHPVQDELKDWGSWFTDELDCYRLDAIKHIFPW 239
 Db 183 kawdewdtengnydylnyadxdmhpevineinrgwvwyantlnldgrldavkhiqfs 242

Qy 240 YTSQWVRHOREADQDLFVVGGEYKDDVGALEFYLDENWMSLFDVPLNIFYRASQOG 299
 Db 243 fmrnwlgvrgtgnlfavaeywkdgalenylskntwmsafdvplhynlyqasnsg 302

Qy 300 GSYDMRNILRSLVPAHPMHAVTFVDNHDTPQGESLESWADWFKPLAYATILTRGGYP 359
 Db 303 gnydmrnlngtlvqrhpshtvfdvnhdtgpgaelesfvvgwfkplayatiltreggyp 362

Qy 360 NVFYGDYIGIPNDNISAKKMDIDELLDARONVAYGTQHDYFDHWDVVGWTRGSSSRPNS 419
 Db 363 qvfgydygipsdgvsyrqqldpllkarkqyaygrqhdvfdhwdvlgwtrgnashpns 422

Qy 420 GLATIMSGPGGSKWYVGRQNAQTWTDLTGNNASVTINGDGWGEFFTTNGGSVSYYVN 479
 Db 423 glatimsdpgpgskwmyvgrqkagevwhdtgnrsgtvtngdgwqgfngvngsvvwwk 482

Qy 480 Q 480
 Db 483 r 483

RESULT 6
 AAB29343
 ID AAB29343 standard; Protein: 483 AA.
 AC AAB29343;
 DT 09-FEB-2001 (first entry)
 DE Bacillus sp. mature alpha-amylase SEQ ID NO:2 mutant #13.
 KW Alpha-amylase: AAI-6; AAI-10; DSM 12650; DSM 12651;
 KW alkaline detergent composition; starch liquefaction; textile desizing;
 KW brewing; baking; ethanol production; starch modification; laundry;
 KW dishwashing; surface cleaning; mutant; mutein.
 OS Bacillus sp.
 OS Synthetic.
 XX Key Location/Qualifiers
 FH Misc-difference 204
 FT /note- "Any amino acid other than Val"
 XX WO200060058-A2.
 PN 12-OCT-2000.
 XX 28-MAR-2000; 2000WO-DK00147.
 XX 31-MAR-1999; 99DK-0000438.
 PR 13-APR-1999; 99DK-0000489.
 XX (NOVO) NOVO NORDISK AS.
 XX Outtrup H, Hoeck LH, Nielsen BR, Borchert TV, Nielsen VS;

PI Bisgard-Frantzen H, Svendsen A, Andersen C;
 XX WPI: 2000-686938/67.
 XX New polypeptides having alpha-amylase activity and nucleic acids
 PT encoding the enzymes, useful as a detergent or a dish wash detergent
 PT composition, for textile desizing, for liquefaction of starch, or for
 PT ethanol production -
 XX Claim 21; Page -: 112pp; English.
 XX The invention relates to two novel Bacillus alpha-amylases, AAI-6 from
 CC Bacillus sp. DSM 12650, and AAI-10 from Bacillus sp. DSM 12651, and
 CC nucleic acids encoding them. The novel alpha-amylases (AAB29310-B29311)
 CC have improved wash performance in alkaline detergent solutions (pH 9-11)
 CC and have a temperature optimum in the range 55-65 degrees Celsius at pH
 CC 9.0. The invention also relates to mutants (AAB29318-B29394) of the
 CC novel alpha-amylases having increased thermal stability, particularly at
 CC acidic pH and/or at low Ca2+ concentration. The invention additionally
 CC encompasses active fragments of the novel alpha-amylases, expression
 CC constructs and host cells comprising nucleic acids encoding the
 CC alpha-amylases of the the invention, and the recombinant production of
 CC these enzymes. The alpha-amylases are useful in a detergent composition
 CC or a dishwash detergent composition, in a desizing composition,
 CC for liquefaction of starch, or for ethanol production. In particular,
 CC the alpha-amylases are useful for textile desizing, starch modification
 CC in the pulp and paper industry, for brewing or baking, or as laundry,
 CC dishwashing or hard surface cleaning detergent compositions. They are
 CC especially useful for removing starch stains during washing with a
 CC detergent at alkaline pH. The alpha-amylases are also useful for
 CC producing drinking or industrial ethanol from starch or whole grains.
 CC Sequences AAB29331-B29394 represent the mutant Bacillus alpha-amylases
 CC of the invention.
 CC Note: The present sequence is not shown in the specification, but
 CC is derived from the wild-type Bacillus sp. alpha amylase (AAB29310)
 CC shown on page 105-106.
 XX Sequence 483 AA;
 SQ

Query Match 71.3%; Score 1915.5; DB 21; Length 483;
 Best Local Similarity 69.2%; Pred. NO. 3.7e-150;
 Matches 333; Conservative 62; Mismatches 85; Indels 1; Gaps 1;

Qy 1 DGLNGTMOYVEWHLNDGQHNRLLHDDAAALSDAGITAIWIPPAYKGNQADVCYGYVD 60
 Db 3 dgtngtimgyfewvnpdgqhnrlhnaqnlknagitaipppawkgtsqndvgygyayd 62

Qy 61 LYDLGEFNQKGTVRTKYGTKAQLERAIGLSKNSDINIVYGDVVMNHKMGADFTFAVOAV 120
 Db 63 lydlgefngkgtvrtkgtkaelerairslkanglqvgydvvmnhkggadfterqvavev 122

Qy 121 NPTNRWQDISGAYTIDAWTGFDFSGRNAYSDFKRWRFHFGVWDQ-RYQENHIFRAN 179
 Db 123 npqnrngvsgtyeavtgnfpgngqhsfkwrwyhfdgtdwdqgrqlsnriykfrg 182

Qy 180 TNWNRVDEENGNDYLLGSNIDFSHPVQDELKDWGSWFTDELDCYRLDAIKHIFPW 239
 Db 183 kawdewdtengnydylnyadxdmhpevineinrgwvwyantlnldgrldavkhiqfs 242

Qy 240 YTSQWVRHOREADQDLFVVGGEYKDDVGALEFYLDENWMSLFDVPLNIFYRASQOG 299
 Db 243 fmrnwlgvrgtgnlfavaeywkdgalenylskntwmsafdvplhynlyqasnsg 302

Qy 300 GSYDMRNILRSLVPAHPMHAVTFVDNHDTPQGESLESWADWFKPLAYATILTRGGYP 359
 Db 303 gnydmrnlngtlvqrhpshtvfdvnhdtgpgaelesfvvgwfkplayatiltreggyp 362

Qy 360 NVFYGDYIGIPNDNISAKKMDIDELLDARONVAYGTQHDYFDHWDVVGWTRGSSSRPNS 419
 Db 363 qvfgydygipsdgvsyrqqldpllkarkqyaygrqhdvfdhwdvlgwtrgnashpns 422

Qy 420 GLATIMSGPGGSKWYVGRQNAQTWTDLTGNNASVTINGDGWGEFFTTNGGSVSYYVN 479

```

Db 423 giatmsdpggskwmyvgrkagevwhdltgnrsgtvtlndqdgwgfvgngsvsvvwx 482
QY 480 Q 480
Db 483 r 483

RESULT 7
AAB29372
ID AAB29372 standard; Protein; 483 AA.
XX AC AAB29372;
XX DT 09-FEB-2001 (first entry)
XX DE Bacillus sp. mature alpha-amylase SEQ ID NO:4 mutant #10.
XX KW Alpha-amylase; AAI-6; AAI-10; DSM 12650; DSM 12651;
KW alkaline detergent composition; starch liquefaction; textile desizing;
KW brewing; baking; ethanol production; starch modification; laundry;
KW dishwashing; surface cleaning; mutant; mutein.
XX OS Bacillus sp.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Misc-difference 181
XX FT /note= "Any amino acid other than Arg"
XX PN WO2000060058-A2.
XX PD 12-OCT-2000.
XX PF 28-MAR-2000; 2000WO-DK00147.
XX PR 31-MAR-1999; 99DK-0000438.
XX PR 13-APR-1999; 99DK-0000489.
XX PA (NOVO ) NOVO NORDISK AS.
XX PI Outtrup H, Hoeck LH, Nielsen BR, Borchert TV, Nielsen VS;
PI Bisgaard-Frantzen H, Svendsen A, Andersen C;
XX DR WPI; 2000-686938/67.
XX PS New polypeptides having alpha-amylase activity and nucleic acids
XX PT encoding the enzymes, useful as a detergent or a dish wash detergent
XX PT composition, for textile desizing, for liquefaction of starch, or for
XX PT ethanol production -
XX PS Claim 21; Page -; 112pp; English.
XX CC The invention relates to two novel Bacillus alpha-amylases, AAI-6 from
XX CC Bacillus sp. DSM 12650, and AAI-10 from Bacillus sp. DSM 12651, and
XX CC nucleic acids encoding them. The novel alpha-amylases (AAB29310-B29311)
XX CC have improved wash performance in alkaline detergent solutions (pH 9-11)
XX CC and have a temperature optimum in the range 55-65 degrees Celsius at pH
XX CC 9.0. The invention also relates to mutants (AAB29318-B29394) of the
XX CC novel alpha-amylases having increased thermal stability, particularly at
XX CC acidic pH and/or at low Ca2+ concentration. The invention additionally
XX CC encompasses active fragments of the novel alpha-amylases, expression
XX CC constructs and host cells comprising nucleic acids encoding the
XX CC alpha-amylases of the invention, and the recombinant production of
XX CC these enzymes. The alpha-amylases are useful in a detergent composition
XX CC or a dishwash detergent composition, in a desizing composition,
XX CC for liquefaction of starch, or for ethanol production. In particular,
XX CC the alpha-amylases are useful for textile desizing, starch modification
XX CC in the pulp and paper industry, for brewing or baking, or as laundry,
XX CC dishwashing or hard surface cleaning detergent compositions. They are
XX CC especially useful for removing starchy stains during washing with a
XX CC detergent at alkaline pH. The alpha-amylases are also useful for
XX CC producing drinking or industrial ethanol from starch or whole grains.

```

CC Sequences AAB29331-B29394 represent the mutant Bacillus alpha-amylases of the invention.

CC Note: The present sequence is not shown in the specification, but is derived from the wild-type Bacillus sp. alpha amylase (AAB29311) shown on page 109-110.

XX CC

SQ Sequence 483 AA;

Query Match 71.3%; Score 1915.5; DB 21; Length 483;
 Best Local Similarity 69.2%; Pred. NO. 3.7e-150;
 Matches 333; Conservative 60; Mismatches 87; Indels 1; Gaps 1;

```

QY 1 DGLGTMQVYEHLENDGQHNRLHDDAAALSDAGITAIWIIPPAYKNGSQADVGYGAYD 60
Db 3 dgngtimgyfewnvpndgqhnrlhnnagnaknagitaipppawkgtsqndvgayd 62
QY 61 LYDLGEFNQKGTVRTKYGTKAQLERAIGSLKSNIDINVGDVVMNHKMGADFTFAVCAVOV 120
Db 63 lydlgefngkgtvrtkygkkaelairskangiqygdvmmhkggadttervqavev 122
QY 121 NPTNRWODISGAYTIDAWTGFDFSGRNNAYSDFKRWHFHNGVDWQD-RYQENHIFRFAN 179
Db 123 npqnrnqevsgtyqleawtgfnfpggrgnqghssfkwrwyhfdgtdwdqsrqlanrykfxg 182
QY 180 TNWNRVDEENGNYDYLLGSNIDFESHPEQDELKDWGSWFTDELDDLGYRLDAIKHIPFW 239
Db 183 kawdwevdtengnydylmyadvdmhpevnhelnrvwvyantcldlgfrldavkhkfs 242
QY 240 YTSDWVRHORNEADQDLFVYGEYKDDVGALEFYLDENWEMSLFDVPLNIFYRASQOG 299
Db 243 fmrwdlghvrgtgknlfavayekndlgalenysktnwtmsafdvplhynlyqasns 302
QY 300 GSYDMENILRGSILVEAHPMAVTFVDNHDTPQGESLESWADVDFKPLAYATILTTREGGYP 359
Db 303 gnydmnlngtlvqrhpsnavtfvndhdtgpealesfvqgwfkplayatiltreggyp 362
QY 360 NVFYGDYGYIPNDNISAKKMDIDELIDARQNYAGTQHDYFDHWDVGVWTRGSSSRPNS 419
Db 363 qvfgydygypsdgypsvrqidpilkarqayaygrqdyfdhwdvfgwtregnashpns 422
QY 420 GLATTMSNGPGSKWYVGRQNRAGQTFWDLTGNNAASVTINGDGWGEFTTGGSVSVYVN 479
Db 423 glatmsdpggskwmyvgrkagevwhdmtgnrsgtvtlndqdgwgfvgngsvsvvwx 482
QY 480 Q 480
Db 483 r 483

```

RESULT 8

AAB29325

ID AAB29325 standard; Protein; 483 AA.

XX AC AAB29325;

XX DT 09-FEB-2001 (first entry)

XX DE Bacillus sp. mature alpha-amylase SEQ ID NO:4 mutant, del-D183/G184.

XX KW Alpha-amylase; AAI-6; AAI-10; DSM 12650; DSM 12651;

XX KW alkaline detergent composition; starch liquefaction; textile desizing;

XX KW brewing; baking; ethanol production; starch modification; laundry;

XX KW dishwashing; surface cleaning; mutant; mutein.

XX OS Bacillus sp.

XX OS Synthetic.

XX PN WO2000060058-A2.

XX PD 12-OCT-2000.

XX PF 28-MAR-2000; 2000WO-DK00147.

```

XX 31-MAR-1999; 99DK-0000438.
PR 13-APR-1999; 99DK-0000489.
XX
PA (NOVO ) NOVO NORDISK AS.
XX
PI Outtrup H, Hoeck LH, Nielsen BR, Borchert TV, Nielsen VS;
PI Bisgard-Frantzen H, Svendsen A, Andersen C;
XX
DR WPI; 2000-686938/67.
XX
PT New polypeptides having alpha-amylase activity and nucleic acids
PT encoding the enzymes, useful as a detergent or a dish wash detergent
PT composition, for textile desizing, for liquefaction of starch, or for
PT ethanol production -
XX
PS Claim 20; Page -: 112pp; English.
XX
CC The invention relates to two novel Bacillus alpha-amylases, AAI-6 from
CC Bacillus sp. DSM 12650, and AAI-10 from Bacillus sp. DSM 12651, and
CC nucleic acids encoding them. The novel alpha-amylases (AAB29310-B29311)
CC have improved wash performance in alkaline detergent solutions (pH 9-11)
CC and have a temperature optimum in the range 55-65 degrees Celsius at pH
CC 9.0. The invention also relates to mutants (AAB29318-B29394) of the
CC novel alpha-amylases having increased thermal stability, particularly at
CC acidic pH and/or at low Ca2+ concentration. The invention additionally
CC encompasses active fragments of the novel alpha-amylases, expression
CC constructs and host cells comprising nucleic acids encoding the
CC alpha-amylases of the the invention, and the recombinant production of
CC these enzymes. The alpha-amylases are useful in a detergent composition
CC for a dishwash detergent composition, in a desizing composition,
CC for liquefaction of starch, or for ethanol production. In particular,
CC the alpha-amylases are useful for textile desizing, starch modification
CC in the pulp and paper industry, for brewing or baking, or as laundry,
CC dishwashing or hard surface cleaning detergent compositions. They are
CC especially useful for removing starchy stains during washing with a
CC detergent at alkaline pH. The alpha-amylases are also useful for
CC producing drinking or industrial ethanol from starch or whole grains.
CC Sequences AAB29318-B29330 represent specific embodiments of the mutant
CC Bacillus alpha-amylases of the invention.
CC Note: The present sequence is not shown in the specification, but
CC is derived from the wild-type Bacillus sp. alpha amylase (AAB29311)
CC shown on page 109-110.
XX
XX Sequence 483 AA;

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```

Query Match 71.3%; Score 1914.5; DB 21; Length 483;
Best Local Similarity 69.2%; Pred. No. 4.4e-150;
Matches 333; Conservative 60; Mismatches 87; Indels 1; Gaps 1;

QY 1 DGLNGTMMQYVEWHLNDGQHNRHDDAALSDAGITAIWPPAYKGNQADVGYGAYD 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 3 dgtngtmqyfewvnpdngqwhrlnhnaqnlknagitalwppawkgtsqndvgayd 62
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 LYDIGENQKGTVTKYGTQRAQLERATGSLKSDINIVGDVMMHKGADTEAVQAVQ 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 63 lydigefnqgtvrtkygkaelralrslkangivgygdvmmhkggadtfrvqave 122
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 121 NPTNRWODISGAYTIDAWTGFDFSGRNNAVYSDFKWRWFHENGVDWDO-RYOENHIFRAN 179
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 123 npqnrndevsgtyqlawtgnfnpgnrqnqhsfkwrwyhtdgtddwdsqrlnrylktfrg 182
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 180 TNNWNRVDEENGNDYLLGSIDFSPHEVQDELKDWGSWFFDELDLCYRDLAKKHIPFW 239
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 183 kawdwvdtengnydylymyadvdmhdhevinelnrvgwywviantldgfrldavkhlkfs 242
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 240 YTSQWVRQRNEADQDLFFVGEYKDKDVGALFYLDEMNNWMSLFDVPLNIFYRASQOG 299
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 243 fmrldwlgvrgtgnkfnfavaeywkdngalenylsktnwtmsafdvphlynlqasns 302
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 300 GSYDMRNLGRSLVEAPMHAIVTFVDNHDTPQGESLSWVADWFKPLAYATILRREGY 359
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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DB 303 gnydmrnlngtlvgrhpsavtfdvndhtqpggealesfvqgfkplayatillregyyp 362
QY 360 NVFYGDYVIGIPDNISAKKMDIDELLDARQNYAYGTQHDYEDHNDVVGWTRREGSSRPN 419
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 363 qvfgydygypsdgvsyrqgldp||karqayaygrqndyfdhwdvigtregshapns 422
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 420 GLATIMSGPGGSKWMMYVGRQNAQTWTDLTCNGASVTINGDGMGEFTTNGSGSVSYVN 479
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 423 glatimsdpgpgskwmyvgrckagevwhdmtnrgstvtlqngdgwhgfvgngsvvwwk 482
QY 480 Q 480
DB 483 r 483
DB 483 r 483

```

RESULT 9

AAB29341

ID AAB29341 standard; Protein; 483 AA.

XX

AC AAB29341;

XX

DT 09-FEB-2001 (first entry)

XX

DE Bacillus sp. mature alpha-amylase SEQ ID NO:2 mutant #11.

XX

KW Alpha-amylase; AAI-6; AAI-10; DSM 12650; DSM 12651;

KW alkaline detergent composition; starch liquefaction; textile desizing;

KW brewing; baking; ethanol production; starch modification; laundry;

KW dishwashing; surface cleaning; mutant; mutein.

XX

OS Bacillus sp.

OS Synthetic.

XX

FX Key Location/Qualifiers

FT Misc-difference 204 /note= "Any amino acid other than Val"

FT

XX WO2000060058-A2.

XX 12-OCT-2000.

XX

PF 28-MAR-2000; 2000WO-DK00147.

XX

PR 31-MAR-1999; 99DK-0000438.

PR 13-APR-1999; 99DK-0000489.

XX

PA (NOVO) NOVO NORDISK AS.

XX

PI Outtrup H, Hoeck LH, Nielsen BR, Borchert TV, Nielsen VS;

PI Bisgard-Frantzen H, Svendsen A, Andersen C;

XX

DR WPI; 2000-686938/67.

XX

PT New polypeptides having alpha-amylase activity and nucleic acids

PT encoding the enzymes, useful as a detergent or a dish wash detergent

PT composition, for textile desizing, for liquefaction of starch, or for

PT ethanol production -

XX

PS Claim 21; Page -: 112pp; English.

XX

CC The invention relates to two novel Bacillus alpha-amylases, AAI-6 from

CC Bacillus sp. DSM 12650, and AAI-10 from Bacillus sp. DSM 12651, and

CC nucleic acids encoding them. The novel alpha-amylases (AAB29310-B29311)

CC have improved wash performance in alkaline detergent solutions (pH 9-11)

CC and have a temperature optimum in the range 55-65 degrees Celsius at pH

CC 9.0. The invention also relates to mutants (AAB29318-B29394) of the

CC novel alpha-amylases having increased thermal stability, particularly at

CC acidic pH and/or at low Ca2+ concentration. The invention additionally

CC encompasses active fragments of the novel alpha-amylases, expression

CC constructs and host cells comprising nucleic acids encoding the

CC alpha-amylases of the the invention, and the recombinant production of

CC these enzymes. The alpha-amylases are useful in a detergent composition

CC for a dishwash detergent composition, in a desizing composition,

CC for liquefaction of starch, or for ethanol production. In particular,

CC the alpha-amylases are useful for textile desizing, starch modification

CC in the pulp and paper industry, for brewing or baking, or as laundry,

CC dishwashing or hard surface cleaning detergent compositions. They are

CC especially useful for removing starchy stains during washing with a

CC detergent at alkaline pH. The alpha-amylases are also useful for

CC producing drinking or industrial ethanol from starch or whole grains.

CC Sequences AAB29318-B29330 represent specific embodiments of the mutant

CC Bacillus alpha-amylases of the invention.

CC Note: The present sequence is not shown in the specification, but

CC is derived from the wild-type Bacillus sp. alpha amylase (AAB29311)

CC shown on page 109-110.

XX

XX Sequence 483 AA;

The invention relates to two novel *Bacillus* alpha-amylases, AAI-5 from *Bacillus* sp. DSM 12650, and AAI-10 from *Bacillus* sp. DSM 12651, and *Bacillus* sp. DSM 12650, and AAI-10 from *Bacillus* sp. DSM 12651, and nucleic acids encoding them. The novel alpha-amylases (AAB29310-B29311) have improved wash performance in alkaline detergent solutions (pH 9-11) and have a temperature optimum in the range 55-65 degrees Celsius at pH 9.0. The invention also relates to mutants (AAB29318-B29394) of the novel alpha-amylases having increased thermal stability, particularly at acidic pH and/or at low Ca^{2+} concentration. The invention additionally encompasses active fragments of the novel alpha-amylases, expression constructs and host cells comprising nucleic acids encoding the alpha-amylases of the invention, and the recombinant production of these enzymes. The alpha-amylases are useful in a detergent composition or a dishwash detergent composition, in a desizing composition, for liquefaction of starch, or for ethanol production. In particular, the alpha-amylases are useful for textile desizing, starch modification in the pulp and paper industry, for brewing or baking, or as laundry, dishwashing or hard surface cleaning detergent compositions. They are especially useful for removing starchy stains during washing with a detergent at alkaline pH. The alpha-amylases are also useful for producing drinking or industrial ethanol from starch or whole grains. Sequences AAB29331-B29394 represent the mutant *Bacillus* alpha-amylases of the invention.

CC Note: The present sequence is not shown in the specification, but
 CC is derived from the wild-type Bacillus sp. alpha amylase (AAB29310)
 CC shown on page 105-106.

XX Sequence 483 AA;

Query Match 71.2%; Score 1913.5; DB 21; Length 483;
 Best Local Similarity 69.0%; Pred. No. 5.3e-150;
 Matches 332; Conservative 63; Mismatches 85; Indels 1; Gaps 1;

QY 1 DGLNGTMOYEWHLNDGQHNRLHDDAAALSDAGITAIWIPPAKGNQADVGAYD 60
 DB 3 dgtngtimgyfevwvndgqhnrlhnaqnlknagitaipwawkgtsqndvgayd 62
 QY 61 LYDLGEFNQKGTVRTKYGTKAQLERAIGSLKNDINVDVVMNHNKMGADTFEAVQAVQ 120
 DB 63 lydlgefngkgtvrtkygkkaeleraiskangiqygdvmmhkggadtferqvavev 122
 QY 121 NPTNRQDISGAYTIDAWTGFDFSGRNNAISDFKWRWFHFGVDWDQ-RYQENHIFRFAN 179
 DB 123 npqnrnqvsgtgyeaeawgfnpggrgnqghssfkwrwyhfdgtdwqsrqlsnriykrfg 182
 QY 180 TNNNRVDEENGNDYLLGSNIDFSHPQDELKDWGSWFTDELDDGYRLDAIKHIPW 239
 DB 183 kawdevdteengnydylmvadvdmhpevineInrvvwyantlnldgfrldavkhqfs 242
 QY 240 YTSDWVRHORNEADQDLFVVGWYKDDVGALEFYLDMMWMSLFDVPLNRYFRASQOG 299
 DB 243 fmrnwlgvrgtgnknlfaavaeywxdlgalenyskntwnsafdvplhnylqasng 302
 QY 300 GSYDMRNLRLGSLVZAPHPHIAVTFVDNHDTPQGESLESWADWFKPLAYATILTRGGYP 359
 DB 303 gnydmrnlrlgtlvgrhshavtfvdnhdtpgealesfvqgfkplayatiltreqgyp 362
 QY 360 NYFYGDYGIIPNDNISAKMDIDELLDARONVAYGTHQDFPHDWDVGVTRGSSSRPN 419
 DB 363 qvyfygdygipndnysakmdidelldaronvaygthqdfphdwdvgvtrgsssrpn 422
 QY 420 GLATIMSGPGSKWMYGRQAGOTWTDLTGNGASVTINGDGMGEFTNGGVSIVYNN 479
 DB 423 glatimsgpgskwmygrqagewhdtgnrsgtvtindgvgqffvngsgsvvwwk 482
 QY 480 Q 480
 DB 483 r 483

RESULT 15

AAB29352
 ID AAB29352 standard; Protein; 483 AA.

XX AC AAB29352;

XX DT 09-FEB-2001 (first entry)

XX DE Bacillus sp. mature alpha-amylase SEQ ID NO:2 mutant #22.

XX KW Alpha-amylase; AAI-6; DSM 12650; DSM 12651;
 KW alkaline detergent composition; starch liquefaction; textile desizing;
 KW brewing; baking; ethanol production; starch modification; laundry;
 KW dishwashing; surface cleaning; mutant; muten.

XX OS Bacillus sp.
 XX Synthetic.

XX FH Key Location/Qualifiers

XX FT Misc-difference 267 /note= "Any amino acid other than Lys"

XX PN WO200060058-A2.

XX PD 12-OCT-2000.

XX 28-MAR-2000; 2000WO-DK00147.
 XX 31-MAR-1999; 99DK-0000438.
 PR 13-APR-1999; 99DK-0000489.
 XX (NOVO) NOVO NORDISK AS.
 XX Outtrup H, Hoeck LH, Nielsen BR, Borchert TV, Nielsen VS;
 PI Bisgard-Frantzen H, Svendsen A, Andersen C;
 XX WPI: 2000-686938/67.
 PT New polypeptides having alpha-amylase activity and nucleic acids
 encoding the enzymes, useful as a detergent or a dish wash detergent
 composition, for textile desizing, for liquefaction of starch, or for
 ethanol production -
 PS Claim 21; Page -; 112pp; English.
 CC The invention relates to two novel Bacillus alpha-amylases, AAI-6 from
 Bacillus sp. DSM 12650, and AAI-10 from Bacillus sp. DSM 12651, and
 nucleic acids encoding them. The novel alpha-amylases (AAB29310-B29311)
 have improved wash performance in alkaline detergent solutions (pH 9-11)
 and have a temperature optimum in the range 55-65 degrees Celsius at pH
 9.0. The invention also relates to mutants (AAB29318-B29394) of the
 novel alpha-amylases having increased thermal stability, particularly at
 acidic pH and/or at low Ca²⁺ concentration. The invention additionally
 encompasses active fragments of the novel alpha-amylases, expression
 constructs and host cells comprising nucleic acids encoding the
 alpha-amylases of the invention, and the recombinant production of
 these enzymes. The alpha-amylases are useful in a detergent composition
 or a dishwash detergent composition, in a desizing composition,
 for liquefaction of starch, or for ethanol production. In particular,
 the alpha-amylases are useful for textile desizing, starch modification
 in the pulp and paper industry, for brewing or baking, or as laundry,
 dishwashing or hard surface cleaning detergent compositions. They are
 especially useful for removing starchy stains during washing with a
 detergent at alkaline pH. The alpha-amylases are also useful for
 producing drinking or industrial ethanol from starch or whole grains.
 CC Sequences AAB29331-B29394 represent the mutant Bacillus alpha-amylases
 of the invention.
 CC Note: The present sequence is not shown in the specification, but
 CC is derived from the wild-type Bacillus sp. alpha amylase (AAB29310)
 CC shown on page 105-106.
 XX Sequence 483 AA;

Query Match 71.2%; Score 1913.5; DB 21; Length 483;
 Best Local Similarity 69.0%; Pred. No. 5.3e-150;
 Matches 332; Conservative 63; Mismatches 85; Indels 1; Gaps 1;

QY 1 DGLNGTMOYEWHLNDGQHNRLHDDAAALSDAGITAIWIPPAKGNQADVGAYD 60
 DB 3 dgtngtimgyfevwvndgqhnrlhnaqnlknagitaipwawkgtsqndvgayd 62
 QY 61 LYDLGEFNQKGTVRTKYGTKAQLERAIGSLKNDINVDVVMNHNKMGADTFEAVQAVQ 120
 DB 63 lydlgefngkgtvrtkygkkaeleraiskangiqygdvmmhkggadtferqvavev 122
 QY 121 NPTNRQDISGAYTIDAWTGFDFSGRNNAISDFKWRWFHFGVDWDQ-RYQENHIFRFAN 179
 DB 123 npqnrnqvsgtgyeaeawgfnpggrgnqghssfkwrwyhfdgtdwqsrqlsnriykrfg 182
 QY 180 TNNNRVDEENGNDYLLGSNIDFSHPQDELKDWGSWFTDELDDGYRLDAIKHIPW 239
 DB 183 kawdevdteengnydylmvadvdmhpevineInrvvwyantlnldgfrldavkhqfs 242
 QY 240 YTSDWVRHORNEADQDLFVVGWYKDDVGALEFYLDMMWMSLFDVPLNRYFRASQOG 299
 DB 243 fmrnwlgvrgtgnknlfaavaeywxdlgalenyskntwnsafdvplhnylqasng 302

Qy 300 GSYDMRNLGRSLVEAHPMHAVTFVDNHDTPQGESLESWADWFKPLAYATILTREGGYP 359
Db 303 gnydmrnlngtlvqrhpshtvfvdnhdtpgealesfvqgwfkplayatiltreggyp 362
Qy 360 NVFYGDYIGIPNDNISAKKDMIDELLDARQNYAYGTOHDYEDHWDVVGWTRGSSSRPNS 419
Db 363 qvfygdygipsdgpsyrqqlpdkargqaygrqndyfdhwdvigwtregnashpns 422
Qy 420 GLATIMSNPGGSKWYVGRONAGQTWDLTGNNGASVTINGDGWGEFFFTNGSGSVSVVN 479
Db 423 glatimsdpgpggskwmygrqkagevwhdltgnrsgtvtlnqdgwqffvngsgsvsvvk 482
Qy 480 Q 480
Db 483 r 483

Search completed: November 28, 2001, 16:58:04
Job time: 207 sec

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Date: Nov 28, 2001 5:37 PM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

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gb_est1:AW223346	+	187.50	328.14	4.1e-09	678	! AW223346 EST300357 tomato fruil
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gb_est2:BF011027	+	191.50	334.17	1.9e-09	771	! BF011027 SB233 Sugar Beet germ
gb_est2:BF073204	+	190.00	332.36	2.4e-09	702	! BF073204 PIP2B_G10 Sugar Beet q
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gb_est1:AW223346	+	187.50	328.14	4.1e-09	678	! AW223346 EST300357 tomato fruil
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gb_est2:BF293368	+	195.00	342.74	6.3e-10	616	! BF293368 HVSMF0001E16f Hordeum
gb_est2:BF011027	+	191.50	334.17	1.9e-09	771	! BF011027 SB233 Sugar Beet germ
gb_est2:BF073204	+	190.00	332.36	2.4e-09	702	! BF073204 PIP2B_G10 Sugar Beet q
gb_gss:AO159694	+	188.50	329.07	3.6e-09	743	! AQ159694 mgxb0001I08r CUGI Rice
gb_est1:AW223346	+	187.50	328.14	4.1e-09	678	! AW223346 EST300357 tomato fruil
gb_est1:AO083906	+	179.00	315.74	2.0e-08	495	! AO083906 AO083906 Cryptomeria j
gb_est2:BF293368	+	195.00	342.74	6.3e-10	616	! BF293368 HVSMF0001E16f Hordeum
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90 LeuLysSerAsnAspIleAsnValTyrGlyAspValValMetAsnHisLy 106
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DEFINITION NF016C06D1F1039 Drought Medicago truncatula cDNA clone NF016C06DT
5', mRNA sequence.
ACCESSION BF632036
VERSION BF632036.1 GI:11896194
KEYWORDS EST.
SOURCE barrel medic.
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
REFERENCE 1 (bases 1 to 639)
AUTHORS Torrez-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,

```

```

TITLE
JOURNAL
COMMENT
Contact: May GD
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7391
Fax: 580 221 7380
Email: gdmay@noble.org
Insert Length: 639 Std Error: 0.00
Plate: 016 row: C column: 06
Seq primer: TCACACAGGAACACAGCTATGAC.
FEATURES
Location/Qualifiers
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Percent similarity: 53.219 Percent identity: 30.043
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US-09-590-375-1 x BF632036
Align seg 1/1 to: BF632036 from: 1 to: 639

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176 TTTGGCTTCCTCCT.....CCATCTCAAAGTGTGGTCTCTCAAGGATAT 219
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73 lArgThrLysTyrGlyThrLysAlaGlnLeuGluArgAlaIleGlySerL 90
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107 MetGlyAlaAspPheThrGluAlaValGlnAlaValGlnValAsnProTh 123
346 .....AC 347
123 rAsnArgTrpGlnAspIleSerGlyAlaTyrThrIleAspAlaTrpThrG 140
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173 His_IlePheGlyPheAlaAsnThrAsnTrpAsnTrpArg_ValAspG 188
447 CACGTCGTATTACAG.....TGGCACTGGAACCTCGGATA 481
188 luGluAsnGlyAsnTyrAspTyrLeuLeuGlySerAsnIleAspPheSer 204
482 GTGAGAGAGGC.....TATCAAGCTGCACCTGCACATTGATCATCTC 522
205 HisProGluValGlnAspGluLeuLeuAspTrpGlySerTrpPheThrAs 221
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DEFINITION	NF047G02EC1F1019 Elicited cell culture Medicago truncatula cDNA clone NF047G02EC 5', mRNA sequence.		

ACCESSION	BF648578
VERSION	BF648578.1
KEYWORDS	EST.
	GI:11913708

SOURCE

ORGANISM

Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.

1 (bases 1 to 665)
Torres-Jerez, I., Scott, A. D., Harris, A. R., Gonzales, R. A., Bell, C. J.,
Flodes, H. K., Iman, J. T., Weller, J. W. and May, G. D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation -
Center for Medicago Genomics Research
Unpublished (2000)
Contact: Dixon RA

**Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7302**

Fax: 580 221 7380

Email: radixon@noble.org

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location/quantity	

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/note= vector: bamboo zap; cell wall extracts equivalent to

final concentration. Samples were

24 hours after induction. Equal

time point were pooled and used

BASE COUNT	196 a	131 c	128 g	207 t

ORIGIN

alignment scores.

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Ratio: 1.775      Gaps: 12
Percent Similarity: 52.632      Percent Identity: 29.386

alignment_block:
US-09-590-375-1 x BF648578      ..

Align seg 1/1 to: BF648578 from: 1 to: 665

11 TyrGluTrpHisLeuGluAsnAspGlyGlnHisTrpAsnArgLeuHisAs 27
   :::::||||:   ::|||   |||   ::|||   |||   ::
87 TTCAACTGGGAGTCAAGTACAAAGAGGAGTGTACAACTCTTTTCAGAA 136
   :::::||||:   ::|||   |||   ::|||   |||   ::
27 pAspAlaAlaLeuSerAspAlaGlyIleIleThrAlaIleTrpIleProp 44
   ||:::||||:   ::|||   |||   ::|||   |||   ::
137 CCTCATTCCTGACCTAGCAAACTGCTGSAATTACACATGTTTGGCTTCCTC 186
   ||:::||||:   ::|||   |||   ::|||   |||   ::
44 roAlaTyrlYsGlyAsnSerGlnAlaAspValGlyTyrlYlAlaTyrlAsp 50
   ||   :::::||||:   ::|||   |||   ::|||   |||   ::
187 CR.....CCATCTCAAAGTGTGGTCCTCCTCAAGGATATCTTCCAGGAAGA 230
   ||   :::::||||:   ::|||   |||   ::|||   |||   ::
61 LeuTyrlAspLeuGlyGluPheAsnGlnLysGlyThrValAlaTrhTrLysTy 77
   |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
231 CTTTATGATCTTGAT.....GCATCAAAATA 256
   |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

```

```

77 rGlyThrLysAlaGlnLeuGluArgAlaLleGlySerLeuLysSerAsnA 94
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
257 CGGTTCAAAGAGATGACCTAAAGTCACCTAAATTCAGCTTTCAAAGATAAG 306
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
94 spIleasnValTyrGlyAspValMetAsnHisLysMetGlyAlaAsp 110
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
307 GAATCAATTTGCTAGCTGCATAGTGTATCAACCATAGA..... 344
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
111 PheThrGluAlaValGlnAlaValGlnValAsnProThrAsnArgTrrpG1 127
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
345 .....ACAGCAGAAAGAAA 358
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
127 nAspIleSerGlyAlaTyrThrIleAspAlaTrrpThrGlyPheAspPheS 144
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
359 AGATGATAGAGGCATCTATTGCCCTC.....TTTG 387
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
144 erGlyArgAsnAsnAlaTyrSerAspPheLysTrrpArgTrrp.PheHis.P 160
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
388 AAGGT.....GGGACTCCTGATTCAAAACWTGATTGGGGCCCATCT 428
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
160 heAsnGlyValAspTrrpAspGlnArgTyrGlnGluAsnHis...IlePhe 175
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
429 TTTCAT.....TTGCAAGATGACACTGCTTATTC 457
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
176 ArgPheAlaAsnThrAsnTrrpAsnTrrpArg.ValAspGluGluAsnGlyA 192
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
458 AGA.....TGGCACTGGAAACCTCGATAGTGGAGAGGCG. 491
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192 snTyrAspTyrLeuLeuGlySerAsnIleAspPheSerHisProGluVal 208
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
492 .....TATCAAGCTGCGACCTGCATTTGATCTCAATCCTCAAGTA 533
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
209 GlnAspGluLeuLysAspTrrpGlySerTrrpPheThrAspGluLeuAspLue 225
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
534 CAAAAGAGCTTATCTGAATGGATGAATTTGGCTCAAAACCTGAAATGGATT 583
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
225 uAspGlyTyrArgLeuAspAlaLleLys 234
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584 TTCTGGGTGGAGATTGATTGTTGTCAAA 611

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seq_name: qb_est2:BG581061

seq documentation block.

LOCUS BG581061

DEFINITION EST482791 GV

mRNA sequence

ACCESSION BG581061

VERSION BG581061.1

KEYWORDS EST'.

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SOURCE
ORGANISM
barrel medic.
Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
1 (bases 1 to 558)
REFERENCE
AUTHORS
Fedorova,M., Pierson,B.L., Samac,D.A., Vance,C.P., Gantt,G.S., Town
,C.D., Van Aken,S., Utterback,T., Cho,J. and Fraser,C.M.
ESTs from one month old nitrogen-fixing root nodules of Medicago
truncatula, 2001
JOURNAL
COMMENT
Unpublished (2001)
Contact: Carroll P. Vance
Department of Agronomy and Plant Genetics
University of Minnesota
411 Borlaug Hall, 1991 Upper Buford Circle, St.Paul, MN 55108 USA
Tel: 612 625 5715
Fax: 651-649-5058
Email: vance004@maroon.tc.umn.edu
University of Minnesota name: M382117e TIGR sequence name:
MTCCD78TK More information is available at: http://www.medicago.org
Seq primer: SKmod (CTA gAA CTA gTg gAT CC).
FEATURES
Location/Qualifiers
1..558
/organism="Medicago truncatula"
/cultivar="genotype Al7"
/db_xref="taxon:3880"
/clone="pGVN-63M12"
/clone_lib="GVN"
/tissue_type="N2-fixing root nodules"
/dev_stage="effective root nodules harvested one month
post inoculation with Sinorhizobium meliloti"
/lab_host="E. coli strain XL0LR"
/note="Vector: pBluescript SK-; Site.1: EcoRI; Site.2:
XhoI; cDNA was prepared from polyA+ enriched RNA from
effective root nodules harvested one month post
inoculation with Sinorhizobium meliloti. The cDNA was
directionally ligated into the Uni-ZAP XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-ZAP phage using Ex-Assist
helper phage and propagated in XL0LR cells."
BASE COUNT 169 a 110 c 115 g 163 t 1 others
ORIGIN
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Quality: 211.00 Length: 231
Ratio: 1.744 Gaps: 12
Percent Similarity: 52.381 Percent Identity: 29.004
alignment_block:
us-09-590-375-1 x BG581061 ..
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25 CTCTTTTCAGGAGTTCACCTGGAGTCAAGTATACAAAGGAGGATGATACAA 74
23 nArgLeuHisAspAlaAlaAlaLeuSerAspAlaGlyIleThrAlaI 40
75 CTCTTTTGAAGAACCTCATCTCCTGACCTACCAATGCTGGAAATTACACATG 124
40 leftrpleProAlaTyrLysGlyAsnSerGlnAlaAspValGlyTyr 56
125 TTTGGCTTCTCCT.....CCATCTCAAGTGTGGTCTCTCAAGGATAT 168
57 GlyAlaTyrAspLeuTyrAspLeuGlyGluPheAsnGlnLysGlyThrVa 73
169 CTTCAGGAGAGACTTTTATGATCTTGAT..... 195
73 lafGThrLysTyrGlyThrLysAlaGlnLeuGluArgAlaIleGlySerL 90

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196 .GCATCAAAATACGGTTCAAAGATGACCTAAAGTCACCTAAATTCAGCTT 244
90 eulYSerAsnAspIleAsnValTyrGlyAspValValMetAsnHisLys 106
245 TCAAGATAAAGAAATCAATGTCTAGCTGACATAGTGTATCAACCATAGA 294
107 MetGlyAlaAspPheThrGluAlaValGlnAlaValGlnValAsnProTh 123
295 .....AC 296
123 rAsnArgTrpGlnAspIleSerGlyAlaTyrThrIleAspAlaTrpThrG 140
297 AGCAGAAAGAAAGATCATAGAGGCATCTATTGCTC..... 333
140 lyPheAspPheSerGlyArgAsnAlaTyrSerAspPheLysTrpArg 156
334 .....TTTGAGGT.....GGGACTCCTGATCAAAACCTTGAT 366
157 Trp.PheHis.PheAsnGlyValAspTrpAspGlnArgTyrGlnGluAsn 172
367 TGGGGCCCATCTTTTCAT.....TTGCAAGATGA 395
173 His...IlePheArgPheAlaAsnThrAsnTrpAsnTrpArg.ValaspG 188
396 CACTGCTTATTCAGA.....TGGCACTGGAACCTCGATA 430
188 luGluAsnGlyAsnTyrAspTyrLeuLeuGlySerAsnIleAspPheSer 204
431 GTGGAGAGGC.....TATCAAGCTGCACCTGACATGATCATCTC 471
205 HisProGluValGlnAspGluLeuLysAspTrpGlySerTrpPheThrAs 221
472 AATCTCAAGTACAAAGAGTTATCTGAATGGATGAATGGCTCAAAAC 521
221 pGluLeuAspLeuAspGlyTyrArgLeuAspAlaIle 233
522 TGAATTTGGATNTCTGGTGGAGATTGATTTTGTG 558
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seq_documentation_block:
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DEFINITION NF041C08PLF1056 Phosphate starved leaf Medicago truncatula cDNA
clone NF041C08PL 5', mRNA sequence.
ACCESSION BF637944
VERSION BF637944.1 GI:11902102
KEYWORDS EST.
SOURCE barrel medic.
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
1 (bases 1 to 587)
REFERENCE
AUTHORS
Liu,J., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores
,H.R., Inman,J.T., Weller,J.W., May,G.D. and Harrison,M.J.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula phosphate-starved leaf library
JOURNAL
COMMENT
Unpublished (2000)
Contact: Harrison MJ
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7325
Fax: 580 221 7380
Email: mharrison@noble.org
Insert Length: 587 Std Error: 0.00
Plate: 041 row: C column: 08
Seq primer: TCACACAGGAACACGCTATGAC.
FEATURES
Location/Qualifiers
1..587
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 /clone_lib="Phosphate starved leaf"
 /tissue_type="leaf"
 /dev_stage="trifoliolate"
 /note="Vector: Lambda Zap; At the trifoliolate stage, M. truncatula plants were transplanted to phosphate-free sand and grown for a further 30 days. During this 30 day period, the plants were fertilized twice weekly with 1/2 Hoaglands solution containing only 20uM potassium phosphate. RNA was prepared from above ground tissues."

BASE COUNT 172 a 117 c 119 g 179 t
 ORIGIN

alignment_scores:
 Quality: 211.00 Length: 229
 Ratio: 1.744 Gaps: 12
 Percent Similarity: 52.838 Percent Identity: 29.258
 alignment_block:
 US-09-590-375-1 x BF637944 ..

Align seg 1/1 to: BF637944 from: 1 to: 587

7 MetGlnTyrTyrGluTrpHisLeuGluAsnAspGlyGlnHisTrpAs 23
 ::::||||| ::::||||| ::::||||| ::::||||| ::::|||||
 59 CTCITTCAGGATTCACCTGGGAGTCAAGTAACAAGGAGGATGGTACAA 108
 ::::||||| ::::||||| ::::||||| ::::||||| ::::|||||
 23 nArgLeuHisAspAspAlaAlaLeuSerAspAlaGlyIleThrAlaI 40
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 109 CTCITTTGAAGAACCTCAATTCCTGACCTAGCAATGCTGGAATTCACATG 158
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 40 LeTrpIleProAlaTyrIlysGlyAsnSerGlnAlaAspValGlyTyr 56
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 159 TTTGGCTTCCTCCT.....CAATCTCAAGTGTGGTCCCAAGGATAT 202
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 57 GlyAlaTyrAspLeuTyrAspLeuGlyGluPheAsnGlnLysGlyThrVa 73
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 203 CTTCCAGGAAGACITTAGTACTTGTAT..... 229
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 73 lArgThrLysTyrGlyThrLysAlaGlnLeuGluArgAlaIleGlySerL 90
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 230 .GCATCAAAATACGGTTCAAAAGATGACCTAAAGTCACTAATTCGAGCTT 278
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 90 euLysSerAsnAspIleAsnValTyrGlyAspValValMetAsnHisLys 106
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 279 TCAAGATAAAGGAATCAATTTGCTAGCTGACATAGTATCAACCATAGA 328
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 107 MetGlyAlaAspPheThrGluAlaValGlnAlaValGlnValAsnProTh 123
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 329AC 330
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 123 rAsnArgTrpGlnAspIleSerGlyAlaTyrThrIleAspAlaTrpThrG 140
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 331 AGCAGAAAGAAAGATGATAGAGCATCTATTGGCCTC..... 367
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 140 lYPheAspPheSerGlyArgAsnAsnAlaTyrSerAspPheLysTrpArg 156
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 368TTTGAAGGT.....GGGACTCTGATTCAAAACCTTGAT 400
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 157 Trp.PheHis.PheAsnGlyValAspTrpAspGlnArgTyrGlnGluAsn 172
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 401 TGGGGCCCATCTTCAT.....TTGCAAGAGATGA 429
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 173 His....IlePheArgPheAlaAsnThrAsnTrpAsnTrpArg.ValAspG 188
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 430 CACTGCTTATTCAGA.....TGGCACTGGAAACCTCGATA 464
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 188 luGluAsnGlyAsnTyrAspTyrLeuLeuGlySerAsnIleAspPheSer 204
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 465 GTGGAGAGGC.....TATCAAGCTGCACCTGACATTCATCATCTC 505

205 HisProGluValGlnAspGluLeuLysAspTrpGlySerTrpPheThrAs 221
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 506 AATCTCAAGTACAAAAGAGTATTCTGAATGGATGATTCGCTCAAAAC 555
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 221 pGluLeuAspLeuAspGlyTyrArgLeuAsp 231
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 556 TCAAAATGGATTTCTGCTGGTGGAGATTTGAT 586
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 seq_documentation_block:
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 clone NF077E12EC 5', mRNA sequence.
 ACCESSION BF647599
 VERSION BF647599.1 GI:11912729
 KEYWORDS barrel medic.
 SOURCE Medicago truncatula
 ORGANISM Medicago truncatula
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids I; Fabales; fabaceae; Papilionoideae; Trifolieae;
 Medicago.
 REFERENCE 1 (bases 1 to 635)
 AUTHORS Torres-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,
 Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D.
 TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation -
 Center for Medicago Genomics Research
 JOURNAL Unpublished (2000)
 COMMENT Contact: Dixon RA
 Plant Biology Division
 The Samuel Roberts Noble Foundation
 2510 Sam Noble Parkway, Ardmore, OK 73402, USA
 Tel: 580 221 7302
 Fax: 580 221 7380
 Email: radixon@noble.org
 Insert Length: 635 Std Error: 0.00
 Plate: 077 row: E column: 12
 Seq primer: TCACACAGAAACACAGCTATGAC.
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 /clone_lib="Elicited cell culture"
 /tissue_type="Cell cultures derived from root tissues"
 /dev_stage="Cell suspensions were subcultured every 14
 days. Cells were induced six days after subculture"
 /note="Vector: Lambda Zap; Cells were induced with yeast
 cell wall extracts equivalent to 50ug/ml glucose in the
 final concentration. Samples were taken at 0.5, 1, 12 and
 24 hours after induction. Equal amounts of RNA from each
 time point were pooled and used for mRNA isolation."
 BASE COUNT 183 a 129 c 125 g 197 t 1 others
 ORIGIN
 alignment_scores:
 Quality: 210.00 Length: 226
 Ratio: 1.780 Gaps: 12
 Percent Similarity: 52.212 Percent Identity: 29.646
 alignment_block:
 US-09-590-375-1 x BF647599 ..
 Align seg 1/1 to: BF647599 from: 1 to: 635
 13 TrpHisLeuGluAsnAspGlyGlnHisTrpAsnArgLeuHisAspAspAl 29
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 95 TGGGAGTCAAGTACAAAGAGGAGTGTACACTCTTTGAAGAACCTCAT 144
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 29 aAlaLeuSerAspAlaGlyIleThrAlaIleTrpIleProAlaIat 46
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

```

145 TCCTGACCTAGCAATGCTGGAATTACACATGTTGGCTTCTCCT.... 190
46 yrlYsGlyAsnSerGlnAlaAspValGlyTyrGlyAlaTyrAspLeuTyr 62
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191 ..CCATCTCAAAAGTGTGGTCTCAAGGATATCTCCAGGAAGACTTAT 238
   :::::|||||
63 AspLeuGlyGluPheAsnGlnGlyThrValArgThrLysTyrGlyTh 79
   |||||
239 GATCTTGAT.....GCATCAAAATACGGTTC 264
79 rLysAlaGlnGluArgAlaIleGlySerLeuLysSerAsnAspIleA 96
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265 AAAGATGACCTAAAGTCACTTAATGACGCTTCAAGAGAAAGAAATCA 314
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96 snValTyrGlyAspValValMetAsnHisLysMetGlyAlaAspPheThr 112
   || :::::|||||
315 ATTCTAGCTGACATAGTATCAACCATAGA..... 346
113 GluAlaValGlnAlaValGlnValAsnProThrAsnArgTrpGlnAspII 129
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347 .....ACAGCAGAAAGAAAGATGA 366
129 eSerGlyAlaTyrThrIleAspAlaTrpThrGlyPheAspPheSerGlyA 146
   ||| ||| :::::|||||
367 TAGAGGCATCTATTGCCCTC.....TTTGAAGGT. 394
146 rgAsnAsnAlaTyrSerAspPheLysTrpArgTrp.PheHis.PheAsnG 162
   :::::|||||
395 .....GGGACTCCCTGATTCAAACTTGTATTGGGCCCATCTTTTCAT. 435
162 lyValAspTrpAspGlnArgTyrGlnGluAsnHis.....IlePheArgPhe 177
   ||| :::::|||||
436 .....TTGCAAGATGACACATGCTTATTTCAGA... 462
178 AlaAsnThrAsnTrpAsnTrpArg.ValAspGluGluAsnGlyAsnTyrA 194
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463 .....TGGCACTGAAACCTCGATAGTGGAGAGGCG..... 493
194 spTyrLeuLeuGlySerAsnIleAspPheSerHisProGluValGlnAsp 210
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494 ..TATCAAGCTGCACCTGACATGATCATCTCAATCTCAAGTACAAAAA 541
211 GluLeuLysAspTrpGlySerTrpPheThrAspCluLeuAspLeuAspG1 227
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542 GAGTATATCAATGATGATTTGGCTCAAACTGAATGGATTCTTCTGG 591
227 yTyrArgLeuAspAlaIleLys 234
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592 TTGGAGATTGATTTGTCAAA 613

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seq_name: gb_est1:AW709933

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seq_documentation_block:
LOCUS      AW709933          436 bp      mRNA      EST      25-APR-2000
DEFINITION Neurospora crassa evening cDNA library Neurospora crassa
            cDNA clone d9b06ne 5', mRNA sequence.
ACCESSION  AW709933
VERSION    AW709933.1  GI:7599010
KEYWORDS   EST.
SOURCE     Neurospora crassa.
            Neurospora crassa
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariales; Sordariaceae; Neurospora.
            1 (bases 1 to 436)
            Zhu, H., Lai, H., Kupfer, D., Dunlap, J.C. and Roe, B.A.
            Two Neurospora crassa EST Databases
            Unpublished (1998)
            Other_ESTs: d9b06ne.r1
            Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
            Department of Chemistry and Biochemistry
            Advanced Center for Genome Technology, University of Oklahoma
            620 Parrington Oval, Norman, OK 73019, USA
            Tel: 405 325 4912

```

Fax: 405 325 7762
 Email: broe@ou.edu
 We anticipate the future release of the cDNA clones to the Fungal
 Genetics Stock Center
 Seq primer: Universal Forward Primer
 High quality sequence stop: 424.

FEATURES

Location/Qualifiers
 1..436
 /organism="Neurospora crassa"
 /strain="Strain 30-7 (bd; A)"
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 /clone_lib="Neurospora crassa evening cDNA library"
 /tissue_type="tissue harvested following 22hr growth in
 dark"
 /note="Vector: pBluescript SK-; Site_1: XbaI; Site_2:
 EcoRI; See: Bell-perdersen.D., et al. PNAS 93:13096,1996.
 5' end of cDNA cloned into XbaI site of pBluescript; 3'
 end of cDNA cloned into EcoRI site of pBluescript"
 BASE COUNT 82 a 159 c 93 g 102 t
 ORIGIN

alignment_scores:

Quality: 206.50 Length: 119
 Ratio: 2.950 Gaps: 2
 Percent Similarity: 58.824 Percent Identity: 41.176

alignment_block:

US-09-590-375-1 x AW709933 ..

Align seg 1/1 to: AW709933 from: 1 to: 436

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273 rLeuAspGluMetAsnTrpGluMetSerLeuPheAspValProLeuAsnT 290
   ||| :::::|||||
130 CATCGAATTTATGCACACCGCTGTCTCTCTCGACGTGCAATTAGTCT 179
   :::::|||||
290 yTrAsnPheTyrArg.....AlaSerGln 297
   |||||
180 CCAACTTCTCCGCATCTTTAGCTTCGAAACACCTCCAGCCCTCC 229
   :::::|||||
298 GlnGlyGly.....Serty 302
   |||||
230 ACGGTGGTGGTGGTGGTCTCCCGGATCAGTACGGCAGCGGCACAC 279
   :::::|||||
302 rAspMetArgAsnIleLeuArgGlySerLeuValGluAlaHisPrometh 319
   ||| :::::|||||
280 CGACCTCGCACCTTATTTCGACGACACCTCTGCACTCTGGAACCGCAC 329
   :::::|||||
319 isAlaValThrPheValAspAsnHisAspThrGlnProGlyGluSerLeu 335
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            genomic survey sequence.
ACCESSION  AL153781

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VERSION      AL153781.1  GI:7014700
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SOURCE       African malaria mosquito.
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             Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
             Culicoidae; Anopheles.
REFERENCE    1 (bases 1 to 681)
AUTHORS      Genoscope.
TITLE        Direct Submission
JOURNAL      Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage :
             BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
             - Web : www.genoscope.cns.fr)
REFERENCE    2 (bases 1 to 681)
AUTHORS      Roth,C.W., Brey,P.T., Ke.Z., Collins,F.H. and Weissenbach,J.
TITLE        Direct Submission
JOURNAL      Submitted (16-FEB-2000) BBMI, Institut Pasteur, 25, rue du Dr.
             Roux, Paris 75015, France
COMMENT      This clone is from an A. gambiae BAC library provided by F.H.
             Collins and sequenced by Genoscope in collaboration with the
             Laboratory of Biochem. and Biol. Molec. of Insects, Institut
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22 pAsnArgLeuHisAspAspAlaAlaLeuSerAspAlaGlyIleThrA 39
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39 laileTrpIleProAlaTyrLysGlyAsnSerGlnAla....AspVal 54
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             NaCl treatment Mesembryanthemum crystallinum cDNA clone L48-2786
             5', mRNA sequence.
ACCESSION  BF479139
VERSION    BF479139.1  GI:11549966
KEYWORDS   common ice plant.
SOURCE     Mesembryanthemum crystallinum
ORGANISM   Mesembryanthemum crystallinum
REFERENCE  1 (bases 1 to 712)
AUTHORS    Cushman, J.C.
TITLE      An expressed sequence tag database for the common ice plant,
             Mesembryanthemum crystallinum
JOURNAL    Unpublished (1997)
COMMENT    Contact: Cushman JC
             Department of Biochemistry
             University of Nevada
             MS200, Reno, NV 89557-0014, USA
             Tel: 775-784-1918
             Fax: 775-784-1650
             Email: jcushman@unr.edu
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             FORWARD: T7
             BACKWARD: T3
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 46 yrLysGlyAsnSerGlnAlaAspValGlyTyrGlyAlaIatyrAspLeuTyr 62
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252 laAspGlnAspLeuPheValValGluTyrTrpLysAsp. 265
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LOCUS WHE2156.e10.1202S Triticum turgidum L. var. durum (durum wheat)
DEFINITION whole plant cDNA library Triticum turgidum cDNA clone
WHE2156.e10.120, mRNA sequence.
ACCESSION BF293666
VERSION BF293666.1 GI:11224730
KEYWORDS EST.
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ORGANISM Triticum turgidum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Triticum.
1 (bases 1 to 533)
REFERENCE
AUTHORS Akhunov,E., Anderson,O.D., Chao,S., Chin,A., Choi,D.W., Close,T.J.,
Fenton,R.D., Han,P.S., Hsia,C.C., Kang,Y., Kianian,P., Lazo,G.R.,
Miller,R., Otto,C., Rausch,C.J., Seaton,C.L., Simons,K., Tong,J.C.
and Zhang,D.
The structure and function of the expressed portion of the wheat
durum - Whole plant cDNA library from Triticum turgidum L. var.
durum
JOURNAL Unpublished (2000)
COMMENT Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA

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Copyright (c) 1993-2000 CompuGen Ltd.

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ACCESSION AX137670
VERSION AX137670.1 GI:14273853
KEYWORDS

SOURCE

Bacillus sp. KSM-K38.

ORGANISM

Bacillus sp. KSM-K38.

REFERENCE 1 (bases 1 to 1753)

Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus.

AUTHORS

Endo, K., Igarashi, K., Hayashi, Y., Hagihara, H. and Ozaki, K.

TITLE

Mutant alpha-amylases

JOURNAL

Patent: EP 1065277-A 3 03-JAN-2001;

FEATURES

Location/Qualifiers

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ORIGIN

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ACCESSION AX137672
VERSION AX137672.1 GI:14273855
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Bacillus sp. KSM-K36
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
REFERENCE
1 (bases 1 to 1625)
AUTHORS Endo, K., Igarashi, K., Hayashi, Y., Hagiwara, H. and Ozaki, K.
TITLE Mutant alpha-amylases
JOURNAL Patent: EP 1065277-A 5 03-JAN-2001;
Kao Corporation (JP)
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seq_name: gb_pat:AR104349

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LOCUS AR104349 1455 bp DNA PAT 14-FEB-2001
DEFINITION Sequence 5 from patent US 6093562.
ACCESSION AR104349
VERSION AR104349.1 GI:12817057
KEYWORDS
SOURCE
ORGANISM

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REFERENCE
1 (bases 1 to 1455)
AUTHORS Bisg,ang.rd-Frantzen,H., Svendsen,A. and Borchert,T.Vedel.
TITLE Amylase variants
JOURNAL Patent: US 6093562-A 5 25-JUL-2000;
FEATURES
Location/Qualifiers
1..1455
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BASE COUNT 473 a 227 c 352 g 403 t
ORIGIN

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Unknown.

Unclassified.

REFERENCE

1 (bases 1 to 1455)

AUTHORS Bisg,ang.rd-Frantzen,H., Svendsen,A. and Borchert,T.Vedel.

TITLE Amylase variants

JOURNAL Patent: US 6093562-A 5 25-JUL-2000;

FEATURES Location/Qualifiers

1..1455

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BASE COUNT 473 a 227 c 352 g 403 t

ORIGIN

alignment_scores:

Quality: 1860.50

Ratio: 4.327

Gaps: 2

Percent Similarity: 89.027

Percent Identity: 66.460

alignment_block:

US-09-590-375-1 x AR104349 ..

Align seg 1/1 to: AR104349 from: 1 to: 1455

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17 nAspGlyGlnHisTrpAsnArgLeuHisAspAlaAlaLeuSerA 34
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57 TGATGGCAATCACTGGAATAGATTAAAGATGATGCTAGTAACTAAGAA 106
34 spAlaGlyIleThrAlaIleTrpIleProProAlaTyrLysGlyAsnSer 50
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157 CAAAATGATGGGGTATGGAGCTATGATCTTTATGATTAGGGGAATT 206
67 eAsnGlnLysGlyThrValArgThrLysTyrGlyThrLysAlaGlnLeuG 84
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DEFINITION	Sequence 10 from patent	US 6187576.
		PAT
		16-MAY-2001

ACCESSION AR129913
 VERSION AR129913.1 GI:14117810
 KEYWORDS .
 SOURCE Unknown.
 ORGANISM Unknown.
 Unclassified.
 REFERENCE 1 (bases 1 to 1455)
 AUTHORS Svendsen,A., Borchert,T.Vedel and Bisg.ang.rd-Frantzen,H.
 TITLE .alpha.-amylase mutants
 JOURNAL Patent: US 6187576-A 10 13-FEB-2001;
 FEATURES Location/Qualifiers
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BASE COUNT	473 a	227 c	352 q	403 t
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ORIGIN

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US-09-590-375-1 x AR129913

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117 aValGlnValAsnProThrAsnArgTrpGlnAspIleSerGlyAlaTyrT 134
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seq_documentation_block: 1455 bp DNA PAT 16-MAY-2001
LOCUS AR129918
DEFINITION Sequence 15 from patent US 6187576.
ACCESSION AR129918
VERSION AR129918.1 GI:14117815
KEYWORDS
SOURCE
ORGANISM

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REFERENCE
1 (bases 1 to 1455)
AUTHORS Svendsen,A., Borchert,T,Vedel and Bisg.ang.rd-Frantzen,H.
TITLE .alpha.-amylase mutants
JOURNAL Patent: US 6187576-A 15 13-FEB-2001;
FEATURES
source
1..1455
Location/Qualifiers
BASE COUNT 473 a 227 c 352 g 403 t -
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alignment_scores:
Quality: 1860.50 Length: 483
Ratio: 4.927 Gaps: 2
Percent Similarity: 89.027 Percent Identity: 66.460

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ACCESSION AR143218
VERSION AR143218.1 GI:15104504
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 1455)
AUTHORS
Borchert,T.Vedel, Svendsen,A., Andersen,C., Nielsen,B.,
Nissen,T.Lauesgaard and Kj.ae buttet.ruliff.Sslashedren.
TITLE
.alpha.-amylase mutants
JOURNAL
Patent: US 6204232-A 14 20-MAR-2001;
FEATURES
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LOCUS AB008763 Bacillus sp. gene for amylase, complete cds.

DEFINITION AB008763

ACCESSION AB008763

VERSION AB008763.1 GI:3445479

KEYWORDS amylase.

SOURCE Bacillus sp. (strain:KSM-1378) DNA.

ORGANISM Bacillus sp.

Bacteria; Firmicutes; Bacillus/Clostridium group;

Bacillus/Staphylococcus group; Bacillus.

REFERENCE 1 (bases 1 to 1786)

AUTHORS Hatada,Y.

TITLE Direct Submission

JOURNAL Submitted (10-NOV-1997) to the DBJ/EMBL/GenBank databases. Yuji

Hakada, Kao Corporation, Tochi Research Laboratories; 2606

Akabane, Ichikai, Haga-gun, Tochi 321-3497, Japan

(Tel:0285-68-7400, Fax:0285-68-7403)

REFERENCE 2 (bases 1 to 1786)

AUTHORS Igarashi,K., Hatada,Y., Ikawa,K., Araki,H., Ozawa,T., Kobayashi,T.,

Ozaki,K. and Ito,S.

TITLE Improved thermostability of a Bacillus alpha-amylase by deletion of

an arginine-glycine residue is caused by enhanced calcium binding

JOURNAL Biochem. Biophys. Res. Commun. 248 (2), 372-377 (1998)

MEDLINE 98342096

FEATURES

source Location/Qualifiers

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